

GenCore version 5.1.6  
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OM protein - protein search, using SW model

Run on: February 6, 2004, 11:37:30 ; Search time 41 Seconds  
(without alignments)  
50.328 Million cell updates/sec

Title: US-09-618-577-28  
Perfect score: 68  
Sequence: 1 KTAGTAPTAGNYS 13

Scoring table: BLOSUM62  
Gapop 10.0, Gapext 0.5

Searched: 1107863 seqs, 158726573 residues

Total number of hits satisfying chosen parameters: 1107863

Minimum DB seq length: 0  
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%  
Maximum Match 100%

Listing first 45 summaries

Database:

1: /SIDSI/gcgdata/geneseq/emb1/AA1980.DAT.\*  
2: /SIDSI/gcgdata/geneseq/emb1/AA1981.DAT.\*  
3: /SIDSI/gcgdata/geneseq/emb1/AA1982.DAT.\*  
4: /SIDSI/gcgdata/geneseq/emb1/AA1983.DAT.\*  
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6: /SIDSI/gcgdata/geneseq/emb1/AA1985.DAT.\*  
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12: /SIDSI/gcgdata/geneseq/emb1/AA1991.DAT.\*  
13: /SIDSI/gcgdata/geneseq/emb1/AA1992.DAT.\*  
14: /SIDSI/gcgdata/geneseq/emb1/AA1993.DAT.\*  
15: /SIDSI/gcgdata/geneseq/emb1/AA1994.DAT.\*  
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22: /SIDSI/gcgdata/geneseq/emb1/AA2001.DAT.\*  
23: /SIDSI/gcgdata/geneseq/emb1/AA2002.DAT.\*  
24: /SIDSI/gcgdata/geneseq/emb1/AA2003.DAT.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	68	100.0	13	AA28333	Antigenic syntheti
2	68	100.0	147	AA17911	Peptide CFA/I from
3	68	100.0	170	AA38324	E. coli colonisati
4	54	79.4	10	AA28324	Antigenic syntheti
5	54	79.4	10	AA28334	Antigenic syntheti
6	47	69.1	167	AA50340	ERIC CS4 pilus Csa
7	41	60.3	537	AA641863	Arabidopsis thalia
8	41	60.3	569	AA641862	Arabidopsis thalia
9	41	60.3	577	AA641861	Arabidopsis thalia

10	41	60.3	1379	22	ABB68940	Drosophila melanog
11	40	58.8	57	22	AAU65565	Propionibacterium
12	40	58.8	263	22	AAU39542	Propionibacterium
13	40	58.8	348	21	AA20258	Arabidopsis thalia
14	40	58.8	362	21	AA20257	Arabidopsis thalia
15	40	58.8	362	22	AAE02530	Arabidopsis thalia
16	40	58.8	374	21	AA20256	Arabidopsis thalia
17	40	58.8	685	21	AA20255	Arabidopsis thalia
18	40	58.8	745	21	AA20254	Arabidopsis thalia
19	40	58.8	951	21	AA20253	Arabidopsis thalia
20	39	57.4	60	22	AAU56836	Propionibacterium
21	39	57.4	60	22	AAU62420	Propionibacterium
22	39	57.4	333	14	AA31019	Grass pollen aller
23	39	57.4	333	20	AA25681	Grass pollen aller
24	39	57.4	376	19	AAW81744	M. tuberculosis im
25	39	57.4	376	19	AAW64377	Mycobacterium tube
26	39	57.4	376	20	AAV39174	M. tuberculosis an
27	39	57.4	376	20	AAV39031	M. tuberculosis re
28	39	57.4	1291	19	AAW59912	Human gene 241-enc
29	38	55.9	152	24	AAW01187	Human secreted pro
30	38	55.9	153	21	AAW0141	Ebola virus glycop
31	38	55.9	295	22	AAW01253	B. subtilis live h
32	38	55.9	363	22	AAU01253	Human protein bequ
33	38	55.9	556	22	AAW5184	Ebola virus glycop
34	38	55.9	676	21	AAV70074	Ebola virus strain
35	38	55.9	676	22	AAE00706	Ebola virus glycop
36	38	55.9	676	22	AAW0133	Chimeric filovirus
37	38	55.9	676	24	AAU18477	Human ORF996
38	38	55.9	733	21	AAU18472	Chimeric filovirus
39	38	55.9	747	24	AAU18472	Drosophila melanog
40	38	55.9	1744	22	AAW62890	Human novel polype
41	38	55.9	1744	22	AAU00090	Human polypeptide
42	37	54.4	125	24	AAU003622	Mycobacterium tube
43	37	54.4	140	22	AAU32425	Mycobacterium tube
44	37	54.4	344	18	AAW32357	Mycobacterium tube
45	37	54.4	344	18	AAW32357	Mycobacterium tube

# ALIGNMENTS

RESULT 1	AA28333	standard; peptide; 13 AA.
AC	AA28333;	
XX	25-MAR-2003 (updated)	
DT	24-MAR-1993 (first entry)	
XX	Antigenic synthetic peptide contg. B-cell epitope 124.	
XX	CFA/I pilus protein; vaccine; bacterial; viral; infection; mammal.	
KW	Synthetic.	
OS	WO9219263-A1.	
XX	12-NOV-1992	
XX	13-MAY-1991; 91WO-US03328.	
XX	24-APR-1991; 91US-0690485.	
XX	(USSA ) US SEC OF ARMY.	
XX	Boedeker EC, Cassels FJ, Jarboe D, Reid RH, Setterstrom JA;	
XX	WPI; 1992-398530/48.	
XX	Protection against entero-pathogenic organisms - comprises oral	
XX	admin. of compsn. consisting of synthetic peptide contg. CFA-I	
XX	pilus protein T-cell epitope(s) and/or B-cell epitope(s)	

PT encapsulated in biodegradable polymeric matrix  
 XX  
 PS Claim 36; Page 76; 121pp; English.  
 XX  
 CC The sequence is that of an antigenic synthetic peptide contg. CFA/I  
 CC plus protein B-cell epitopes which may be encapsulated within a  
 CC biodegradable polymeric matrix consisting of poly(DL-lactide-co-  
 CC glycolide) having a relative ratio between the amt. of lactide and  
 CC glycolide components within the range of 48:52 to 52:48 for use as a  
 CC vaccine for the immunisation of a human or other mammal against  
 CC infection by enteropathogenic organisms. This provides extremely  
 CC effective protection against bacterial or viral infections in the  
 CC tissue of a mammal. It protects against bacteria including *Salmonella*  
 CC typhi, *Shigella sonnei*, *S. flexneri*, *S. dysenteriae*, *S. boydii*,  
 CC *E. coli*, *Vibrio cholerae*, *Yersinia*, *Staphylococcus*, *Clostridium* and  
 CC campylobacter. Viruses protected against include hepatitis A,  
 CC rotaviruses, polio virus, HIV, Herpes simplex virus types 1 and 2,  
 CC varicella-zoster virus, Epstein-Barr virus and cytomegaloviruses  
 CC See also AAR28315-R28334.  
 CC (Updated on 25-MAR-2003 to correct PN field.)  
 CC  
 SQ Sequence 13 AA;  
 QY Query Match 100.0%; Score 68; DB 13; Length 13;  
 Best Local Similarity 100.0%; Pred. No. 5.2e-05;  
 Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 DB 1 KTAGTAPTAGNYS 13  
 QY 1 KTAGTAPTAGNYS 13  
 DB 1 KTAGTAPTAGNYS 13

RESULT 2  
 AAM17911  
 ID AAM17911 standard; peptide; 147 AA.  
 XX  
 AC AAM17911;  
 XX  
 DT 25-JUL-1997 (first entry)  
 XX  
 DE Peptide CFA/I from denatured protein subunits of *E. coli* fimbriae.  
 XX  
 KW Immunisation; fimbrial protein; colonisation factor antigen;  
 KM antibody.  
 XX  
 OS *Escherichia coli*.  
 OS Synthetic.  
 XX  
 PN WO9638171-A1.  
 XX  
 PD 05-DEC-1996.  
 XX  
 PF 03-JUN-1996; 96WO-US08730.  
 XX  
 PR 02-JUN-1995; 95US-0460617.  
 XX  
 PA (USSA ) US DEPT OF THE ARMY.  
 XX  
 PI Anderson J, Carter JM, Casseels F;  
 XX  
 DR WPI; 1997-034101/03.  
 XX  
 PT New consensus peptide from fimbrial proteins of the *E. coli* family  
 PT CS4-CFA/I - and denatured fimbrial proteins, used for immunisation  
 PT against infection by bacteria of this family  
 XX  
 PS Disclosure; Page 4; 17pp; English.  
 XX  
 CC The present sequence is a peptide from the denatured protein subunit  
 CC of fimbriae from CFA/I. Many of the denatured proteins give rise to  
 CC antibodies that are reactive with proteins of other strains as shown  
 CC by precipitation studies on nitrocellulose. They are also reactive  
 CC with surface antigens of the fimbriae as shown by agglutination

CC of organisms. They can be used to immunise against disease caused by  
 CC enterotoxigenic *E. coli* of the family CS4-CFA/I. Also antibodies raised  
 CC against the *E. coli* CS4-CFA/I family can be used as diagnostic reagents  
 CC to identify antigens.  
 XX  
 SQ Sequence 147 AA;  
 QY Query Match 100.0%; Score 68; DB 18; Length 147;  
 Best Local Similarity 100.0%; Pred. No. 0.00079;  
 Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 DB 124 KTAGTAPTAGNYS 136  
 QY 1 KTAGTAPTAGNYS 13  
 DB 124 KTAGTAPTAGNYS 136

RESULT 3  
 AAM38341  
 ID AAM38341 standard; Protein; 170 AA.  
 XX  
 AC AAM38341;  
 XX  
 DT 27-MAR-1998 (first entry)  
 XX  
 DE *E. coli* colonisation factor antigen CFAI.  
 XX  
 KW Bacterial colonisation; colonisation factor antigen; CFAI;  
 KW enterotoxigenic *Escherichia coli*; vaccine; diagnosis; research.  
 XX  
 OS *Escherichia coli*.  
 XX  
 PN US5698416-A.  
 XX  
 PD 16-DEC-1997.  
 XX  
 PF 02-JUN-1995; 95US-0460739.  
 XX  
 PR 02-JUN-1995; 95US-0460739.  
 XX  
 PA (USSA ) US SEC OF ARMY.  
 XX  
 PI Bell BA, Casseels FU, Wolf MK;  
 XX  
 DR WPI; 1998-051486/05.  
 DR N-PSDB; AAT96059.  
 XX  
 PT Production of bacterial colonisation factor protein - by expression  
 PT under control of heat-inducible promoter  
 XX  
 PS Example 2; Columns 15-18; 11pp; English.  
 XX  
 CC Production of a protein that affects bacterial colonisation,  
 CC comprises inoculating a broth containing tryptone and yeast extract  
 CC with enteric bacteria containing a DNA sequence encoding the  
 CC protein under the control of a temperature regulated promoter,  
 CC culturing the bacteria, removing the bacteria from the medium and  
 CC recovering the protein. The method is used especially for producing  
 CC the colonisation factor antigen CFAI of enterotoxigenic *E. coli*, i.e.  
 CC the antigen denoted by the present sequence, which may be used in  
 CC vaccines or for diagnostic or research purposes. Growing the  
 CC bacteria at low temperature until the late logarithmic phase  
 CC increases the yield of the protein.  
 CC  
 SQ Sequence 170 AA;  
 QY Query Match 100.0%; Score 68; DB 19; Length 170;  
 Best Local Similarity 100.0%; Pred. No. 0.00094;  
 Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 DB 147 KTAGTAPTAGNYS 159  
 QY 1 KTAGTAPTAGNYS 13  
 DB 147 KTAGTAPTAGNYS 159

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RESULT 4
AAR28324
ID AAR28324 standard; peptide; 10 AA.
XX
AC AAR28324;
XX
DT 25-MAR-2003 (updated)
DT 24-MAR-1993 (first entry)
XX
DE Antigenic synthetic peptide contg. T-cell epitope 126.
XX
KW CFA/I pilus protein; vaccine; bacterial; viral; infection; mammal.
XX
OS Synthetic.
XX
PN WO9219263-A1.
XX
PD 12-NOV-1992.
XX
PF 13-MAY-1991; 91WO-US03328.
XX
PR 24-APR-1991; 91US-0690485.
XX
PA (USSA ) US SEC OF ARMY.
XX
PI Boedeker EC, Cassels FJ, Jarboe D, Reid RH, Setterstrom JA;
XX
PS WPI; 1992-398530/48.
XX
PT Protection against entero-pathogenic organisms - comprises oral
PT admin. of compsn. consisting of synthetic peptide contg. CFA-I
PT pilus protein T-cell epitope(s) and/or B-cell epitope(s)
PT encapsulated in biodegradable polymeric matrix
XX
XX
XX Claim 23; Page 76; 121pp; English.
XX
PS The sequence is that of an antigenic synthetic peptide contg. CFA/I
CC plus protein T-cell epitopes which may be encapsulated within a
CC biodegradable polymeric matrix consisting of poly(DL-lactide-co-
CC glycolide) having a relative ratio between the amt. of lactide and
CC glycolide components within the range of 48:52 to 52:48 for use as a
CC vaccine for the immunisation of a human or other mammal against
CC infection by enteropathogenic organisms. This provides extremely
CC effective protection against bacterial or viral infections in the
CC tissue of a mammal. It protects against bacteria including Salmonella
CC typhi, Shigella sonnei, S. flexneri, S. dysenteriae, S. boydii,
CC E.coli, Vibrio cholera, Yersinia, staphylococcus, clostridium and
CC campylobacter. Viruses protected against include hepatitis A,
CC rotaviruses, polio virus, HIV, Herpes simplex virus types 1 and 2,
CC Varicella-Zoster virus, Epstein-Barr virus and cytomegaloviruses
CC See also AAR28315-R28334.
CC (Updated on 25-MAR-2003 to correct PN field.)
XX
SQ Sequence 10 AA;
XX
QY Query Match 79.4%; Score 54; DB 13; Length 10;
Best Local Similarity 100.0%; Pred. NO. 0.0094;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
DB 3 AGTAPTAGNY 12
1 AGTAPTAGNY 10
XX
RESULT 5
AAR28334
ID AAR28334 standard; peptide; 10 AA.
XX
AC AAR28334;
XX
DT 25-MAR-2003 (updated)
DT 24-MAR-1993 (first entry)
XX

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XX
DE Antigenic synthetic peptide contg. B-cell epitope 127.
XX
KW CFA/I pilus protein; vaccine; bacterial; viral; infection; mammal.
XX
OS Synthetic.
XX
PN WO9219263-A1.
XX
PD 12-NOV-1992.
XX
PF 13-MAY-1991; 91WO-US03328.
XX
PR 24-APR-1991; 91US-0690485.
XX
PA (USSA ) US SEC OF ARMY.
XX
PI Boedeker EC, Cassels FJ, Jarboe D, Reid RH, Setterstrom JA;
XX
PS WPI; 1992-398530/48.
XX
PT Protection against entero-pathogenic organisms - comprises oral
PT admin. of compsn. consisting of synthetic peptide contg. CFA-I
PT pilus protein T-cell epitope(s) and/or B-cell epitope(s)
PT encapsulated in biodegradable polymeric matrix
XX
XX
XX Claim 35; Page 76; 121pp; English.
XX
PS The sequence is that of an antigenic synthetic peptide contg. CFA/I
CC plus protein B-cell epitopes which may be encapsulated within a
CC biodegradable polymeric matrix consisting of poly(DL-lactide-co-
CC glycolide) having a relative ratio between the amt. of lactide and
CC glycolide components within the range of 48:52 to 52:48 for use as a
CC vaccine for the immunisation of a human or other mammal against
CC infection by enteropathogenic organisms. This provides extremely
CC effective protection against bacterial or viral infections in the
CC tissue of a mammal. It protects against bacteria including Salmonella
CC typhi, Shigella sonnei, S. flexneri, S. dysenteriae, S. boydii,
CC E.coli, Vibrio cholera, Yersinia, staphylococcus, clostridium and
CC campylobacter. Viruses protected against include hepatitis A,
CC rotaviruses, polio virus, HIV, Herpes simplex virus types 1 and 2,
CC Varicella-Zoster virus, Epstein-Barr virus and cytomegaloviruses.
CC See also AAR28315-R28333.
CC (Updated on 25-MAR-2003 to correct PN field.)
XX
SQ Sequence 10 AA;
XX
QY Query Match 79.4%; Score 54; DB 13; Length 10;
Best Local Similarity 100.0%; Pred. NO. 0.0094;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
DB 4 GTAPTAGNYS 13
1 GTAPTAGNYS 10
XX
RESULT 6
AAM50340
ID AAM50340 standard; Protein; 167 AA.
XX
AC AAM50340;
XX
DT 18-FEB-2002 (first entry)
XX
DE ETEC CS4 pilus CsaB fimbrial structural protein.
XX
KW CS4 pilus; enterotoxigenic; ETEC; csa operon; CsaB; fimbrial;
XX vaccine; diarrhoea; antibacterial; antidiarrhetic.
XX
OS Escherichia coli.
XX
XX
XX Key Location/Qualifiers
FH Peptide 1..23
FT

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FT Protein /label= Signal\_peptide  
FT 24..167  
XX /label= Mature\_protein  
PN MO200181582-A2.  
XX  
PD 01-NOV-2001.  
XX  
PF 20-APR-2001; 2001WO-US12914.  
XX  
PR 20-APR-2000; 2000US-198686P.  
XX  
PA (UTMA-) UNIV MARYLAND BALTIMORE.  
XX  
PI Altdoun Z, Levine MM, Barry EM;  
XX  
DR MPI: 2002-049280/06.  
DR N-PSDB; AAI70760, AAI70780.  
XX  
PT New nucleotide sequence, useful as immunogenic agent for generating  
PT immune response against recombinant product of the operon, comprises  
PT csa operon which encodes enterotoxigenic Escherichia coli-CS4 pili  
XX  
PS Claim 4; Page 50; 81pp; English.  
XX  
CC The present sequence is that of fimbrial structural protein CsaB  
CC of enterotoxigenic Escherichia coli (ETEC) strain E11881A. CsaB is  
CC encoded by the csaB gene (see AAI70760) of the E. coli E11881A csa  
CC operon. This operon has 5 contiguous genes, csaA-csaE, which encode  
CC the synthesis of ETEC-CS4 pili. It has been expressed in attenuated  
CC Shigella strain CVD1204 guaba, constructing the Shigella expressing  
CC CS4 fimbriae vaccine strain CVD1204 (pgA2-CS4). The CsaB protein  
CC has a calculated mol. wt. of 17343.9 and a theoretical pI of 6.56.  
CC It shares homology with other ETEC fimbriae proteins. Recombinant  
CC CsaA-CsaE polypeptides are used in claimed immunogenic compositions  
CC to generate an immune response in a subject. These prevent ETEC  
CC colonisation, and hence protect against diarrhoea.  
XX  
SQ Sequence 167 AA:  
  
Query Match 69.1%; Score 47; DB 23; Length 167;  
Best Local Similarity 75.0%; Pred. No. 3.5;  
Matches 9; Conservative 0; Mismatches 3; Indels 0; Gaps 0;  
  
QY 2 TAGTAPTAGNYS 13  
DB 145 TTQAAPTGNYS 156  
  
RESULT 7  
AAG41863  
ID AAG41863 standard; Protein; 537 AA.  
XX  
AC AAG41863;  
XX  
XX 18-OCT-2000 (first entry)  
XX  
DE Arabidopsis thaliana protein fragment SEQ ID NO: 52138.  
XX  
XX Protein identification; signal transduction pathway; metabolic pathway;  
XX hybridisation assay; genetic mapping; gene expression control; promoter;  
XX termination sequence.  
XX  
OS Arabidopsis thaliana.  
XX  
PN EP1033405-A2.  
XX  
PD 06-SEP-2000.  
XX  
PF 25-FEB-2000; 2000EP-0301439.  
XX  
PR 25-FEB-1999; 99US-0121825.  
PR 05-MAR-1999; 99US-0123180.

PR 09-MAR-1999; 99US-0123548.  
PR 23-MAR-1999; 99US-0125788.  
PR 25-MAR-1999; 99US-0126264.  
PR 29-MAR-1999; 99US-0126785.  
PR 01-APR-1999; 99US-0127462.  
PR 06-APR-1999; 99US-0128234.  
PR 08-APR-1999; 99US-0128714.  
PR 16-APR-1999; 99US-0129845.  
PR 19-APR-1999; 99US-0130077.  
PR 21-APR-1999; 99US-0130449.  
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PR 28-APR-1999; 99US-0131449.  
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PR 04-MAY-1999; 99US-0132484.  
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PR 06-MAY-1999; 99US-0132486.  
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PR 07-MAY-1999; 99US-0132863.  
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PR 14-MAY-1999; 99US-0134218.  
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PR 14-MAY-1999; 99US-0134221.  
PR 14-MAY-1999; 99US-0134370.  
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PR 24-MAY-1999; 99US-0135629.  
PR 25-MAY-1999; 99US-0136021.  
PR 27-MAY-1999; 99US-0136392.  
PR 28-MAY-1999; 99US-0136782.  
PR 01-JUN-1999; 99US-0137222.  
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PR 04-JUN-1999; 99US-0137502.  
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PR 10-JUN-1999; 99US-0138540.  
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PR 14-JUN-1999; 99US-0139119.  
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PR 23-JUN-1999; 99US-0140353.  
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PR 24-JUN-1999; 99US-0140695.  
PR 28-JUN-1999; 99US-0140823.  
PR 29-JUN-1999; 99US-0140991.  
PR 30-JUN-1999; 99US-0141287.  
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PR 06-JUL-1999; 99US-0142390.  
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PR 26-JUL-1999; 99US-0145224.  
PR 27-JUL-1999; 99US-0145276.  
PR 27-JUL-1999; 99US-0145913.  
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XX OS Arabidopsis thaliana.  
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DT 18-OCT-2000 (first entry)

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XX Protein identification; signal transduction pathway; metabolic pathway;  
KW hybridisation assay; genetic mapping; gene expression control; promoter;  
KW termination sequence.

XX Arabidopsis thaliana.

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 PR 22-OCT-1999; 99US-0160989.  
 PR 25-OCT-1999; 99US-0161404.  
 PR 25-OCT-1999; 99US-0161405.  
 PR 25-OCT-1999; 99US-0161406.  
 PR 26-OCT-1999; 99US-0161359.  
 PR 26-OCT-1999; 99US-0161360.  
 PR 26-OCT-1999; 99US-0161361.  
 PR 28-OCT-1999; 99US-0161920.  
 PR 28-OCT-1999; 99US-0161921.  
 PR 28-OCT-1999; 99US-0161922.  
 PR 29-OCT-1999; 99US-0161993.  
 PR 29-OCT-1999; 99US-0162142.

Query Match 60.3%; Score 41; DB 21; Length 577;  
 Best Local Similarity 61.5%; Pred. No. 1.5e+02;  
 Matches 8; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

QY 1 KTACTAPTAGNYS 13  
 Db 539 RTGTAPGPNYS 551

## RESULT 10

ABBE6940  
 ID ABBE6940 standard; Protein, 1379 AA.

XX ABBE6940;

XX 26-MAR-2002 (first entry)

XX Drosophila melanogaster polypeptide SEQ ID NO 33612.

XX Drosophila; developmental biology; cell signalling; insecticide;  
 pharmaceutical.

XX Drosophila melanogaster.

XX WO200171042-A2.

XX 27-SEP-2001.

XX 23-MAR-2001; 2001WO-US09231.

XX 23-MAR-2000; 2000US-191637P.

PR 11-JUL-2000; 2000US-0614150.

XX (PEKE ) PE CORP NY.

XX Venter JC, Adams M, Li PWD, Myers EW;

XX MPI; 2001-656860/75.

XX N-PSDB; ABL13043.

PT New isolated nucleic acid detection reagent for detecting 1000 or more  
 genes from Drosophila and for elucidating cell signalling and cell-cell  
 interactions -

XX Dislosure; SEQ ID NO 33612; 21pp + Sequence Listing; English.

CC The invention relates to an isolated nucleic acid detection reagent  
 CC capable of detecting 1000 or more genes from Drosophila. The invention is  
 CC useful in developmental biology and in elucidating cell signalling and  
 CC cell-cell interactions in higher eukaryotes for the development of  
 CC insecticides, therapeutics and pharmaceutical drugs. The invention  
 CC discloses genomic DNA sequences (ABL16176-ABL30511), expressed DNA  
 CC sequences (ABL01840-ABL16175) and the encoded proteins  
 CC (ABBS7737-ABBT2072).



CC The sequence data for this patent did not form part of the printed  
CC specification, but was obtained in electronic format directly from WIPO  
CC at ftp.wipo.int/pub/published\_pct\_sequences.

XX Sequence 1379 AA;

Query Match 60.3%; Score 41; DB 22; Length 1379;  
Best Local Similarity 63.6%; Pred. No. 3.9e+02;  
Matches 7; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

OY 2 TAGTAPTAGN 12  
Db 1049 SAGTSPTASSY 1059

## RESULT 11

AAU65565  
ID AAU65565 standard; Protein; 57 AA.

XX AAU65565;

XX 27-FEB-2002 (first entry)

DE Propionibacterium acnes immunogenic protein #26461.

XX SAPHO syndrome; synovitis; acne; pustulosis; hypertosis; osteomyelitis;  
KW uveitis; endophthalmitis; bone; joint; central nervous system; ELISA;  
KW inflammatory lesion; acne vulgaris; enzyme linked immunosorbent assay;  
KW dermatological; osteopathic; neuroprotectant.

XX Propionibacterium acnes.

XX WO200181581-A2.

XX 01-NOV-2001.

XX 20-APR-2001; 2001WO-US12865.

XX 21-APR-2000; 2000US-199047P.

XX 02-JUN-2000; 2000US-208841P.

XX 07-JUL-2000; 2000US-216747P.

XX (CORI-) CORIXA CORP.

XX Skeiky YAM, Persing DH, Mitcham JL, Wang SS, Bhactia A;  
PI L'maisonmeuve J, Zhang Y, Jen S, Carter D;

XX WPI; 2001-616774/71.

XX N-PSDB; AAS59676.

XX Propionibacterium acnes polypeptides and nucleic acids useful for  
PT vaccinating against and diagnosing infections, especially useful for  
PT treating acne vulgaris -

XX Example 1; SEQ ID No 26760; 1069pp; English.

XX  
CC Sequences AAU39105-AAU68017 represent Propionibacterium acnes immunogenic  
CC polypeptides. The proteins and their associated DNA sequences are used in  
CC the treatment, prevention and diagnosis of medical conditions caused by  
CC P. acnes. The disorders include SAPHO syndrome (synovitis, acne,  
CC pustulosis, hypertosis and osteomyelitis), uveitis and endophthalmitis.  
CC P. acnes is also involved in infections of bone, joints and the central  
CC nervous system, however it is particularly involved in the inflammatory  
CC lesions associated with acne vulgaris. A method for detecting the  
CC presence or absence of P. acnes in a patient comprises contacting a  
CC sample with a binding agent that binds to the proteins of the invention  
CC and determining the amount of bound protein in the sample. The  
CC polypeptides may be used as antigens in the production of antibodies  
CC specific for P. acnes proteins. These antibodies can be used to  
CC downregulate expression and activity of P. acnes polypeptides and  
CC therefore treat P. acnes infections. The antibodies may also be used as  
CC diagnostic agents for determining P. acnes presence, for example, by  
CC enzyme linked immunosorbent assay (ELISA).

CC Note: The sequence data for this patent did not form part of the printed  
CC specification, but was obtained in electronic format directly from WIPO  
CC at ftp.wipo.int/pub/published\_pct\_sequences.

XX Sequence 57 AA;

Query Match 58.8%; Score 40; DB 22; Length 57;  
Best Local Similarity 88.9%; Pred. No. 16;  
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 2 TAGTAPTAG 10  
Db 19 TASTAPTAG 27

## RESULT 12

AAU39542  
ID AAU39542 standard; Protein; 263 AA.

XX AAU39542;

XX 13-FEB-2002 (first entry)

DE Propionibacterium acnes immunogenic protein #438.

XX SAPHO syndrome; synovitis; acne; pustulosis; hypertosis; osteomyelitis;  
KW uveitis; endophthalmitis; bone; joint; central nervous system; ELISA;  
KW inflammatory lesion; acne vulgaris; enzyme linked immunosorbent assay;  
KW dermatological; osteopathic; neuroprotectant.

XX Propionibacterium acnes.

XX WO200181581-A2.

XX 01-NOV-2001.

XX 20-APR-2001; 2001WO-US12865.

XX 21-APR-2000; 2000US-199047P.

XX 02-JUN-2000; 2000US-208841P.

XX 07-JUL-2000; 2000US-216747P.

XX (CORI-) CORIXA CORP.

XX Skeiky YAM, Persing DH, Mitcham JL, Wang SS, Bhactia A;  
PI L'maisonmeuve J, Zhang Y, Jen S, Carter D;

XX WPI; 2001-616774/71.

XX N-PSDB; AAS59507.

XX Propionibacterium acnes polypeptides and nucleic acids useful for  
PT vaccinating against and diagnosing infections, especially useful for  
PT treating acne vulgaris -

XX Example 1; SEQ ID No 737; 1069pp; English.

XX  
CC Sequences AAU39105-AAU68017 represent Propionibacterium acnes immunogenic  
CC polypeptides. The proteins and their associated DNA sequences are used in  
CC the treatment, prevention and diagnosis of medical conditions caused by  
CC P. acnes. The disorders include SAPHO syndrome (synovitis, acne,  
CC pustulosis, hypertosis and osteomyelitis), uveitis and endophthalmitis.  
CC P. acnes is also involved in infections of bone, joints and the central  
CC nervous system, however it is particularly involved in the inflammatory  
CC lesions associated with acne vulgaris. A method for detecting the  
CC presence or absence of P. acnes in a patient comprises contacting a  
CC sample with a binding agent that binds to the proteins of the invention  
CC and determining the amount of bound protein in the sample. The  
CC polypeptides may be used as antigens in the production of antibodies  
CC specific for P. acnes proteins. These antibodies can be used to  
CC downregulate expression and activity of P. acnes polypeptides and  
CC therefore treat P. acnes infections. The antibodies may also be used as  
CC diagnostic agents for determining P. acnes presence, for example, by  
CC enzyme linked immunosorbent assay (ELISA).

CC Note: The sequence data for this patent did not form part of the printed  
CC specification, but was obtained in electronic format directly from WIPO  
CC at ftp.wipo.int/pub/published\_pat\_sequences.

XX Sequence 263 AA;

Query Match 58.8%; Score 40; DB 22; Length 263;  
Best Local Similarity 63.6%; Pred. No. 89;  
Matches 7; Conservative 2; Mismatches 0; Gaps 0;

QY 3 ACTAPTAGNYS 13  
|||:|:|:  
Db 174 AGTSPTAAQYA 184

## RESULT 13

ID AAG20258 strand: Protein; 348 AA.

XX AAG20258;

DT 17-OCT-2000 (first entry)

XX Arabidopsis thaliana protein fragment SEQ ID NO: 22375.

KW Protein identification; signal transduction pathway; metabolic pathway;  
hybridization assay; genetic mapping; gene expression control; promoter;  
termination sequence.

XX Arabidopsis thaliana.

PN EP1033405-A2.

XX 06-SEP-2000.

PF 25-FEB-2000; 2000EP-0301439.

XX 25-FEB-1999; 99US-0121825.

PR 05-MAR-1999; 99US-0123180.

PR 09-MAR-1999; 99US-0123548.

PR 23-MAR-1999; 99US-0125788.

PR 25-MAR-1999; 99US-0126264.

PR 29-MAR-1999; 99US-0126785.

PR 01-APR-1999; 99US-0127462.

PR 06-APR-1999; 99US-0128234.

PR 08-APR-1999; 99US-0128714.

PR 16-APR-1999; 99US-0129845.

PR 19-APR-1999; 99US-0130077.

PR 21-APR-1999; 99US-0130449.

PR 23-APR-1999; 99US-0130510.

PR 28-APR-1999; 99US-0131449.

PR 30-APR-1999; 99US-0132048.

PR 04-MAY-1999; 99US-0132407.

PR 04-MAY-1999; 99US-0132484.

PR 05-MAY-1999; 99US-0132485.

PR 06-MAY-1999; 99US-0132486.

PR 07-MAY-1999; 99US-0132487.

PR 11-MAY-1999; 99US-0132863.

PR 14-MAY-1999; 99US-0134256.

PR 14-MAY-1999; 99US-0134218.

PR 14-MAY-1999; 99US-0134219.

PR 14-MAY-1999; 99US-0134221.

PR 14-MAY-1999; 99US-0134370.

PR 18-MAY-1999; 99US-0134368.

PR 19-MAY-1999; 99US-0134941.

PR 20-MAY-1999; 99US-0135124.

PR 21-MAY-1999; 99US-0135353.

PR 24-MAY-1999; 99US-0135629.

PR 25-MAY-1999; 99US-0136021.

PR 27-MAY-1999; 99US-0136392.

PR 28-MAY-1999; 99US-0136782.

PR 01-JUN-1999; 99US-0137222.

PR 03-JUN-1999; 99US-0137528.

PR 04-JUN-1999; 99US-0137502.

PR 07-JUN-1999; 99US-0137724.

PR 08-JUN-1999; 99US-0138094.

PR 10-JUN-1999; 99US-0138540.

PR 10-JUN-1999; 99US-0138847.

PR 14-JUN-1999; 99US-0139119.

PR 16-JUN-1999; 99US-0139452.

PR 16-JUN-1999; 99US-0139453.

PR 17-JUN-1999; 99US-0139492.

PR 18-JUN-1999; 99US-0139454.

PR 18-JUN-1999; 99US-0139455.

PR 18-JUN-1999; 99US-0139456.

PR 18-JUN-1999; 99US-0139457.

PR 18-JUN-1999; 99US-0139458.

PR 18-JUN-1999; 99US-0139459.

PR 18-JUN-1999; 99US-0139460.

PR 18-JUN-1999; 99US-0139461.

PR 18-JUN-1999; 99US-0139462.

PR 18-JUN-1999; 99US-0139463.

PR 18-JUN-1999; 99US-0139750.

PR 18-JUN-1999; 99US-0139763.

PR 22-JUN-1999; 99US-0139817.

PR 23-JUN-1999; 99US-0139889.

PR 23-JUN-1999; 99US-0140353.

PR 24-JUN-1999; 99US-0140354.

PR 24-JUN-1999; 99US-0140695.

PR 28-JUN-1999; 99US-0140823.

PR 29-JUN-1999; 99US-0140991.

PR 30-JUN-1999; 99US-0141287.

PR 01-JUL-1999; 99US-0141842.

PR 01-JUL-1999; 99US-0142154.

PR 02-JUL-1999; 99US-0142055.

PR 06-JUL-1999; 99US-0142390.

PR 08-JUL-1999; 99US-0142803.

PR 09-JUL-1999; 99US-0142920.

PR 12-JUL-1999; 99US-0142977.

PR 13-JUL-1999; 99US-0143542.

PR 14-JUL-1999; 99US-0143624.

PR 15-JUL-1999; 99US-0144005.

PR 16-JUL-1999; 99US-0144085.

PR 16-JUL-1999; 99US-0144086.

PR 19-JUL-1999; 99US-0144325.

PR 19-JUL-1999; 99US-0144326.

PR 19-JUL-1999; 99US-0144331.

PR 20-JUL-1999; 99US-0144632.

PR 20-JUL-1999; 99US-0144684.

PR 21-JUL-1999; 99US-0144814.

PR 21-JUL-1999; 99US-0145086.

PR 21-JUL-1999; 99US-0145088.

PR 22-JUL-1999; 99US-0145089.

PR 22-JUL-1999; 99US-0145087.

PR 22-JUL-1999; 99US-0145089.

PR 22-JUL-1999; 99US-0145192.

PR 23-JUL-1999; 99US-0145145.

PR 23-JUL-1999; 99US-0145218.

PR 23-JUL-1999; 99US-0145224.

PR 26-JUL-1999; 99US-0145276.

PR 27-JUL-1999; 99US-0145913.

PR 27-JUL-1999; 99US-0145918.

PR 27-JUL-1999; 99US-0145919.

PR 28-JUL-1999; 99US-0145951.

PR 02-AUG-1999; 99US-0146386.

PR 02-AUG-1999; 99US-0146388.

PR 02-AUG-1999; 99US-0146389.

PR 03-AUG-1999; 99US-0147038.

PR 04-AUG-1999; 99US-0147204.

PR 04-AUG-1999; 99US-0147302.

PR 05-AUG-1999; 99US-0147192.

PR 05-AUG-1999; 99US-0147260.  
PR 06-AUG-1999; 99US-0147303.  
PR 06-AUG-1999; 99US-0147416.  
PR 09-AUG-1999; 99US-0147493.  
PR 09-AUG-1999; 99US-0147935.  
PR 10-AUG-1999; 99US-0148171.  
PR 11-AUG-1999; 99US-0148319.  
PR 12-AUG-1999; 99US-0148341.  
PR 13-AUG-1999; 99US-0148565.  
PR 13-AUG-1999; 99US-0148684.  
PR 15-AUG-1999; 99US-0149368.  
PR 17-AUG-1999; 99US-0149175.  
PR 18-AUG-1999; 99US-0149426.  
PR 20-AUG-1999; 99US-0149722.  
PR 20-AUG-1999; 99US-0149723.  
PR 20-AUG-1999; 99US-0149929.  
PR 23-AUG-1999; 99US-0149902.  
PR 23-AUG-1999; 99US-0149920.  
PR 25-AUG-1999; 99US-0150566.  
PR 26-AUG-1999; 99US-0150884.  
PR 27-AUG-1999; 99US-0151065.  
PR 27-AUG-1999; 99US-0151066.  
PR 27-AUG-1999; 99US-0151080.  
PR 30-AUG-1999; 99US-0151303.  
PR 31-AUG-1999; 99US-0151438.  
PR 01-SEP-1999; 99US-0151930.  
PR 07-SEP-1999; 99US-0152363.  
PR 10-SEP-1999; 99US-0153070.  
PR 13-SEP-1999; 99US-0153758.  
PR 15-SEP-1999; 99US-0154018.  
PR 16-SEP-1999; 99US-0154039.  
PR 20-SEP-1999; 99US-0154779.  
PR 22-SEP-1999; 99US-0155139.  
PR 23-SEP-1999; 99US-0155486.  
PR 24-SEP-1999; 99US-0155659.  
PR 28-SEP-1999; 99US-0156458.  
PR 29-SEP-1999; 99US-0156596.  
PR 04-OCT-1999; 99US-0157117.  
PR 05-OCT-1999; 99US-0157753.  
PR 06-OCT-1999; 99US-0157865.  
PR 07-OCT-1999; 99US-0158029.  
PR 08-OCT-1999; 99US-0158232.  
PR 12-OCT-1999; 99US-0158369.  
PR 13-OCT-1999; 99US-0159293.  
PR 13-OCT-1999; 99US-0159294.  
PR 13-OCT-1999; 99US-0159295.  
PR 14-OCT-1999; 99US-0159329.  
PR 14-OCT-1999; 99US-0159330.  
PR 14-OCT-1999; 99US-0159331.  
PR 14-OCT-1999; 99US-0159637.  
PR 14-OCT-1999; 99US-0159638.  
PR 16-OCT-1999; 99US-0159584.  
PR 16-OCT-1999; 99US-0160741.  
PR 21-OCT-1999; 99US-0160767.  
PR 21-OCT-1999; 99US-0160778.  
PR 21-OCT-1999; 99US-0160770.  
PR 21-OCT-1999; 99US-0160815.  
PR 21-OCT-1999; 99US-0160814.  
PR 22-OCT-1999; 99US-0160980.  
PR 22-OCT-1999; 99US-0160981.  
PR 22-OCT-1999; 99US-0160989.  
PR 25-OCT-1999; 99US-0161404.  
PR 25-OCT-1999; 99US-0161405.  
PR 25-OCT-1999; 99US-0161406.  
PR 26-OCT-1999; 99US-0161359.  
PR 26-OCT-1999; 99US-0161360.  
PR 26-OCT-1999; 99US-0161361.  
PR 28-OCT-1999; 99US-0161920.  
PR 28-OCT-1999; 99US-0161992.  
PR 28-OCT-1999; 99US-0161993.  
PR 29-OCT-1999; 99US-0162142.  
Query Match 58.8%; Score 40; DB 21; Length 348;

Best Local Similarity 72.7%; Pred. No. 1.2e+02;  
Matches 8; Conservative 1; Mismatches 2; Indels 0; Gaps 0;  
Oy 1 KTAGTAPTACN 11  
Db 290 KTAGPAPTYGH 300

## RESULT 14

AAG20257

ID AAG20257 standard; Protein; 362 AA.

XX AAG20257;

XX 17-OCT-2000 (first entry)

DE Arabidopsis thaliana protein fragment SEQ ID NO: 22374.

XX

KW Protein identification; signal transduction pathway; metabolic pathway;

KM hybridisation assay; genetic mapping; gene expression control; promoter;

XX termination sequence.

OS Arabidopsis thaliana.

XX

PN EP1033405-A2.

XX

PD 06-SEP-2000.

XX

PF 25-FEB-2000; 2000EP-0301439.

XX

PR 25-FEB-1999; 99US-0121825.

XX

PR 05-MAR-1999; 99US-0123180.

XX

PR 09-MAR-1999; 99US-0123548.

XX

PR 23-MAR-1999; 99US-0125788.

XX

PR 25-MAR-1999; 99US-0126264.

XX

PR 29-MAR-1999; 99US-0126785.

XX

PR 01-APR-1999; 99US-0127462.

XX

PR 06-APR-1999; 99US-0128234.

XX

PR 08-APR-1999; 99US-0128714.

XX

PR 16-APR-1999; 99US-0129845.

XX

PR 19-APR-1999; 99US-0130077.

XX

PR 21-APR-1999; 99US-0130449.

XX

PR 23-APR-1999; 99US-0130510.

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PR 23-APR-1999; 99US-0130891.

XX

PR 28-APR-1999; 99US-0131449.

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PR 30-APR-1999; 99US-0132068.

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PR 30-APR-1999; 99US-0132407.

XX

PR 04-MAY-1999; 99US-0132484.

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PR 05-MAY-1999; 99US-0132485.

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PR 06-MAY-1999; 99US-0132486.

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PR 07-MAY-1999; 99US-0132487.

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PR 11-MAY-1999; 99US-0132863.

PR 14-MAY-1999; 99US-0134218.

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PR 14-MAY-1999; 99US-0134221.

PR 14-MAY-1999; 99US-0134370.

PR 16-MAY-1999; 99US-0134768.

PR 19-MAY-1999; 99US-0134941.

PR 20-MAY-1999; 99US-0135124.

PR 21-MAY-1999; 99US-0135353.

PR 24-MAY-1999; 99US-0135629.

PR 25-MAY-1999; 99US-0136021.

PR 27-MAY-1999; 99US-0136382.

PR 28-MAY-1999; 99US-0136782.

PR 01-JUN-1999; 99US-0137222.

PR 03-JUN-1999; 99US-0137528.

PR 04-JUN-1999; 99US-0137502.

PR 07-JUN-1999; 99US-0137724.

PR 08-JUN-1999; 99US-0138094.

PR 10-JUN-1999; 99US-0138540.

PR 10-JUN-1999; 99US-0138847.

PR 14-JUN-1999; 99US-0139119.

PR 16-JUN-1999; 99US-0139452.  
PR 16-JUN-1999; 99US-0139453.  
PR 17-JUN-1999; 99US-0139452.  
PR 18-JUN-1999; 99US-0139454.  
PR 18-JUN-1999; 99US-0139455.  
PR 18-JUN-1999; 99US-0139456.  
PR 18-JUN-1999; 99US-0139457.  
PR 18-JUN-1999; 99US-0139458.  
PR 18-JUN-1999; 99US-0139459.  
PR 18-JUN-1999; 99US-0139460.  
PR 18-JUN-1999; 99US-0139461.  
PR 18-JUN-1999; 99US-0139462.  
PR 18-JUN-1999; 99US-0139463.  
PR 18-JUN-1999; 99US-0139750.  
PR 18-JUN-1999; 99US-0139753.  
PR 21-JUN-1999; 99US-0139817.  
PR 22-JUN-1999; 99US-0139899.  
PR 23-JUN-1999; 99US-0140353.  
PR 23-JUN-1999; 99US-0140354.  
PR 24-JUN-1999; 99US-0140695.  
PR 28-JUN-1999; 99US-0140823.  
PR 29-JUN-1999; 99US-0140991.  
PR 30-JUN-1999; 99US-0141287.  
PR 01-JUL-1999; 99US-0141842.  
PR 02-JUL-1999; 99US-0142154.  
PR 06-JUL-1999; 99US-0142390.  
PR 08-JUL-1999; 99US-0142803.  
PR 09-JUL-1999; 99US-0142920.  
PR 12-JUL-1999; 99US-0142977.  
PR 13-JUL-1999; 99US-0143542.  
PR 14-JUL-1999; 99US-0143624.  
PR 15-JUL-1999; 99US-0144005.  
PR 16-JUL-1999; 99US-0144085.  
PR 16-JUL-1999; 99US-0144086.  
PR 19-JUL-1999; 99US-0144325.  
PR 19-JUL-1999; 99US-0144331.  
PR 19-JUL-1999; 99US-0144332.  
PR 19-JUL-1999; 99US-0144333.  
PR 19-JUL-1999; 99US-0144334.  
PR 19-JUL-1999; 99US-0144335.  
PR 20-JUL-1999; 99US-0144352.  
PR 20-JUL-1999; 99US-0144632.  
PR 20-JUL-1999; 99US-0144684.  
PR 21-JUL-1999; 99US-0144814.  
PR 21-JUL-1999; 99US-0145086.  
PR 21-JUL-1999; 99US-0145088.  
PR 22-JUL-1999; 99US-0145087.  
PR 22-JUL-1999; 99US-0145087.  
PR 22-JUL-1999; 99US-0145089.  
PR 22-JUL-1999; 99US-0145192.  
PR 23-JUL-1999; 99US-0145145.  
PR 23-JUL-1999; 99US-0145218.  
PR 23-JUL-1999; 99US-0145224.  
PR 26-JUL-1999; 99US-0145276.  
PR 27-JUL-1999; 99US-0145913.  
PR 27-JUL-1999; 99US-0145918.  
PR 27-JUL-1999; 99US-0145919.  
PR 27-JUL-1999; 99US-0145919.  
PR 28-JUL-1999; 99US-0145951.  
PR 02-AUG-1999; 99US-0146386.  
PR 02-AUG-1999; 99US-0146388.  
PR 02-AUG-1999; 99US-0146389.  
PR 03-AUG-1999; 99US-0147038.  
PR 04-AUG-1999; 99US-0147204.  
PR 04-AUG-1999; 99US-0147302.  
PR 05-AUG-1999; 99US-0147192.  
PR 05-AUG-1999; 99US-0147260.  
PR 06-AUG-1999; 99US-0147303.  
PR 06-AUG-1999; 99US-0147416.  
PR 09-AUG-1999; 99US-0147493.  
PR 09-AUG-1999; 99US-0147935.  
PR 10-AUG-1999; 99US-0148171.  
PR 11-AUG-1999; 99US-0148319.

PR 12-AUG-1999; 99US-0148341.  
PR 13-AUG-1999; 99US-0148565.  
PR 13-AUG-1999; 99US-0148565.  
PR 16-AUG-1999; 99US-0148684.  
PR 17-AUG-1999; 99US-0149368.  
PR 17-AUG-1999; 99US-0149175.  
PR 18-AUG-1999; 99US-0149426.  
PR 20-AUG-1999; 99US-0149722.  
PR 20-AUG-1999; 99US-0149723.  
PR 20-AUG-1999; 99US-0149929.  
PR 23-AUG-1999; 99US-0149902.  
PR 23-AUG-1999; 99US-0149930.  
PR 25-AUG-1999; 99US-0150566.  
PR 26-AUG-1999; 99US-0150884.  
PR 27-AUG-1999; 99US-0151065.  
PR 27-AUG-1999; 99US-0151066.  
PR 27-AUG-1999; 99US-0151080.  
PR 30-AUG-1999; 99US-0151303.  
PR 31-AUG-1999; 99US-0151438.  
PR 01-SEP-1999; 99US-0151930.  
PR 07-SEP-1999; 99US-0152363.  
PR 10-SEP-1999; 99US-0153070.  
PR 13-SEP-1999; 99US-0153758.  
PR 15-SEP-1999; 99US-0154018.  
PR 16-SEP-1999; 99US-0154029.  
PR 20-SEP-1999; 99US-0154779.  
PR 22-SEP-1999; 99US-0155139.  
PR 23-SEP-1999; 99US-0155486.  
PR 24-SEP-1999; 99US-0155659.  
PR 28-SEP-1999; 99US-0156458.  
PR 29-SEP-1999; 99US-0156596.  
PR 04-OCT-1999; 99US-0157117.  
PR 05-OCT-1999; 99US-0157553.  
PR 06-OCT-1999; 99US-0157865.  
PR 07-OCT-1999; 99US-0158029.  
PR 08-OCT-1999; 99US-0158237.  
PR 12-OCT-1999; 99US-0158369.  
PR 13-OCT-1999; 99US-0158293.  
PR 13-OCT-1999; 99US-0159295.  
PR 14-OCT-1999; 99US-0159295.  
PR 14-OCT-1999; 99US-0159329.  
PR 14-OCT-1999; 99US-0159330.  
PR 14-OCT-1999; 99US-0159331.  
PR 14-OCT-1999; 99US-0159637.  
PR 14-OCT-1999; 99US-0159638.  
PR 14-OCT-1999; 99US-0159638.  
PR 18-OCT-1999; 99US-0159584.  
PR 21-OCT-1999; 99US-0160741.  
PR 21-OCT-1999; 99US-0160767.  
PR 21-OCT-1999; 99US-0160768.  
PR 21-OCT-1999; 99US-0160770.  
PR 21-OCT-1999; 99US-0160814.  
PR 21-OCT-1999; 99US-0160815.  
PR 22-OCT-1999; 99US-0160981.  
PR 22-OCT-1999; 99US-0160981.  
PR 22-OCT-1999; 99US-0160989.  
PR 22-OCT-1999; 99US-0161404.  
PR 25-OCT-1999; 99US-0161405.  
PR 25-OCT-1999; 99US-0161406.  
PR 25-OCT-1999; 99US-0161359.  
PR 26-OCT-1999; 99US-0161360.  
PR 26-OCT-1999; 99US-0161361.  
PR 26-OCT-1999; 99US-0161920.  
PR 28-OCT-1999; 99US-0161992.  
PR 28-OCT-1999; 99US-0161993.  
PR 29-OCT-1999; 99US-0162142.

Query Match 58.8%; Score 40; DB 21; Length 362;  
Best Local Similarity 72.7%; Pred. No. 1.3e+02;  
Matches 8; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 KTAGTAPTGN 11  
DB 304 KTAGPAPTYGH 314

Key	Location/Qualifiers
Region	13..63
	/note="Conserved domain"
MO200135726-A1.	
25-MAY-2001.	
14-NOV-2000; 2000MO-US31418.	
17-NOV-1999; 99US-0166228.	
17-APR-2000; 2000US-0197899.	
22-AUG-2000; 2000US-0227439.	
(MENDEL-) MENDEL BIOTECHNOLOGY INC.	
(HEAR/) HEARD J.	
(RATC/) RATCLIFFE O.	
(CREE/) CREELMAN R.	
(JIANG/) JIANG C.	
(PINE/) PINEDA O.	
(REUB/) REUBER L.	
(ADAM/) ADAM L.	
Heard J, Ratcliffe O, Creelman R, Jiang C, Pineda O, Reuber L, Adam L;	
WPI; 2001-335978/35.	
N-PSDB; AAD06499.	
Nucleic acids encoding plant transcription factor polypeptides, useful for altering the pathogen resistance characteristics of plants, e.g. corn, potato and cotton plants -	
Claim 4; Page 129-131; 134pp; English.	
The present sequence is Arabidopsis thaliana transcription factor homologue. The transcription factors are used to alter the structure and developmental characteristics of plants such as soybean, wheat, corn, potato, cotton, rice, oilseed rape, sunflower, alfalfa, sugarcane, turf, banana, blackberry, blueberry, strawberry, raspberry, carrot, cantaloupe, cauliflower, cucumber, coffee, eggplant, grapes, mango, lettuce, honeydew, melon, onion, papaya, pepper, pineapple, spinach, squash, sweet corn, tobacco, tomato, pear, watermelon, roseaceous fruits and vegetable brassicae. The transcription factors are specifically useful for modifying traits associated with plant's pathogen tolerance such as alterations in cell wall composition, trichome number or structure, callose induction, phytoalexin induction, and alterations in the cell death response. Transgenic plants expressing these transcription factors are more tolerant to biotrophic or necrotrophic pathogens such as fungi, bacteria, molluscs, viruses, nematodes and parasitic higher plants. The transcription factors are also used in gene therapy.	
Sequence 362 AA;	

Qy	1	KTACTAAPTACN	11	.	.
Db	304	KTACAPAPTYGH	314		

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Search completed: February 6, 2004, 11:38:26
Job time : 42 secs

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GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: February 6, 2004, 11:37:31 ; Search time 21 Seconds  
(without alignments)  
26.192 Million cell updates/sec

Title: US-09-618-577-28  
Perfect score: 68  
Sequence: 1 KTAGTAPTAGNYS 13

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 328717 seqs, 42310858 residues

Total number of hits satisfying chosen parameters: 328717

Minimum DB seq length: 0  
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%  
Maximum Match 100%

Listing first 45 summaries

Database : Issued Patents AA:\*  
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5: /cgn2\_6/ptodata/1/1aa/PTUS.COMB.pep:\*  
6: /cgn2\_6/ptodata/1/1aa/backfile1.pep:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	68	100.0	147	5 PCT-US96-08730-9	Sequence 9, Appli
2	68	100.0	170	1 US-08-460-739-3	Sequence 3, Appli
3	68	100.0	170	2 US-08-483-101-11	Sequence 11, Appli
4	39	57.4	175	4 US-09-252-991A-30331	Sequence 30331, A
5	39	57.4	376	4 US-09-056-556-202	Sequence 202, App
6	39	57.4	376	4 US-09-072-586-197	Sequence 197, App
7	38	55.9	328	4 US-09-252-991A-26586	Sequence 26586, A
8	38	55.9	363	4 US-09-173-300-20	Sequence 20, Appli
9	38	55.9	501	4 US-09-252-991A-32936	Sequence 32936, A
10	38	55.9	676	4 US-08-760-615-2	Sequence 2, Appli
11	37	54.4	311	4 US-09-252-991A-30797	Sequence 30797, A
12	37	54.4	344	3 US-08-818-112-69	Sequence 69, Appli
13	37	54.4	344	4 US-08-818-111-70	Sequence 70, Appli
14	37	54.4	344	4 US-09-056-556-69	Sequence 69, Appli
15	37	54.4	344	4 US-09-072-596-70	Sequence 70, Appli
16	36	52.9	203	4 US-09-252-991A-22678	Sequence 22678, A
17	36	52.9	230	4 US-09-252-991A-28638	Sequence 28638, A
18	36	52.9	239	4 US-09-372-422A-42	Sequence 42, Appli
19	36	52.9	275	4 US-09-314-701-28	Sequence 28, Appli
20	36	52.9	508	4 US-09-252-991A-17386	Sequence 17386, A
21	36	52.9	680	1 US-08-542-363-4	Sequence 4, Appli
22	36	52.9	680	1 US-09-100-089-4	Sequence 4, Appli
23	36	52.9	680	1 US-09-670-827-4	Sequence 4, Appli
24	36	52.9	1620	1 US-08-542-363-2	Sequence 2, Appli
25	36	52.9	1620	3 US-09-100-089-2	Sequence 2, Appli
26	36	52.9	1620	4 US-09-670-827-2	Sequence 2, Appli
27	35.5	52.2	513	3 US-09-097-889-15	Sequence 15, Appli

28	35.5	52.2	513	4 US-09-098-079-15	Sequence 15, Appli
29	35	51.5	188	4 US-09-252-991A-24789	Sequence 24789, A
30	35	51.5	245	4 US-09-325-932A-89	Sequence 89, Appli
31	35	51.5	389	4 US-09-513-057C-23	Sequence 23, Appli
32	35	51.5	411	4 US-09-252-991A-28696	Sequence 28696, A
33	35	51.5	427	4 US-09-252-991A-17391	Sequence 17391, A
34	35	51.5	451	3 US-09-412-102-8	Sequence 8, Appli
35	35	51.5	451	3 US-09-217-787-8	Sequence 8, Appli
36	35	51.5	455	3 US-09-412-102-6	Sequence 6, Appli
37	35	51.5	455	3 US-09-412-102-10	Sequence 10, Appli
38	35	51.5	455	3 US-09-217-787-6	Sequence 6, Appli
39	35	51.5	455	3 US-09-217-787-10	Sequence 10, Appli
40	35	51.5	532	4 US-09-252-991A-30492	Sequence 30492, A
41	35	51.5	1132	4 US-09-198-452A-466	Sequence 466, App
42	35	51.5	1179	4 US-09-252-991A-17895	Sequence 17895, A
43	34	50.0	34	2 US-08-640-847C-16	Sequence 16, Appli
44	34	50.0	36	3 US-09-100-600A-4	Sequence 4, Appli
45	34	50.0	36	3 US-09-100-600A-10	Sequence 10, Appli

## ALIGNMENTS

RESULT 1  
PCT-US96-08730-9  
Sequence 9, Application PC/TUS9608730  
GENERAL INFORMATION:  
APPLICANT: Casseels, Frederick  
APPLICANT: Anderson, Jeffrey  
TITLE OF INVENTION: Methods of Raising Antibodies Against E.  
TITLE OF INVENTION: Coli of the Family CSF-CFA/1  
NUMBER OF SEQUENCES: 15  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Glenna Hendicks  
STREET: P.O. Box 2509  
CITY: Fairfax  
STATE: VA  
COUNTRY: USA  
ZIP: 22031  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: PCT/US96/08730  
FILING DATE: 03-JUN-1996  
CLASSIFICATION:  
ATTORNEY/AGENT INFORMATION:  
NAME: Hendicks, Glenna  
REGISTRATION NUMBER: 32,535  
REFERENCE/DOCKET NUMBER: PCT/US96/08730  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (703) 591-4470  
TELEFAX: (703) 591-4428  
INFORMATION FOR SEQ ID NO: 9:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 147 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: unknown  
MOLECULE TYPE: peptide  
HYPOTHEICAL: NO  
ANTI-SENSE: NO  
FRAGMENT TYPE: internal  
PCT-US96-08730-9  
Query Match 100.0%; Score 68; DB 5; Length 147;  
Best Local Similarity 100.0%; Pred. No. 0.00012;  
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 KTAGTAPTAGNYS 13

Db 124 KTAGTAPTAGNYS 136

## RESULT 2

US-08-460-739-3  
Sequence 3, Application US/08460739  
Patent No. 5698416  
GENERAL INFORMATION:  
APPLICANT: Wolf, Marcia K.  
APPLICANT: Casels, Frederick J.  
APPLICANT: Bell, Brian A.  
TITLE OF INVENTION: Improved Methods for Production of  
TITLE OF INVENTION: Antigens Under Control of Temperature-Regulated Promoters  
NUMBER OF SEQUENCES: 5  
CORRESPONDENCE ADDRESS:  
ADDRESSER: Glenna Hendricks  
STREET: 9669 A Main Street  
CITY: Fairfax  
STATE: VA  
COUNTRY: US  
ZIP: 22031  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/460,739  
FILING DATE: 20-APR-1995  
CLASSIFICATION: 514  
ATTORNEY/AGENT INFORMATION:  
NAME: Hendricks, Glenna M.  
REGISTRATION NUMBER: 32,535  
REFERENCE/DOCKET NUMBER: wolf2  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (703) 425-4250  
TELEFAX: (703) 425-2767  
INFORMATION FOR SEQ ID NO: 3:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 170 amino acids  
TYPE: amino acid  
STRANDEDNESS: unknown  
TOPOLOGY: unknown  
MOLECULE TYPE: protein  
HYPOTHETICAL: NO  
AMT-SENSE: NO  
ORIGINAL SOURCE:  
ORGANISM: CFAl protein  
US-08-460-739-3

Query Match 100.0%; Score 68; DB 1; Length 170;

Best Local Similarity 100.0%; Pred. No. 0.00014;  
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KTAGTAPTAGNYS 13  
Db 147 KTAGTAPTAGNYS 159

## RESULT 3

US-08-483-101-11  
Sequence 11, Application US/08483101  
Patent No. 5932715  
GENERAL INFORMATION:  
APPLICANT: Scott, June R.  
APPLICANT: Froehlich, Barbara  
APPLICANT: Caron, Judy  
TITLE OF INVENTION: CS2 Proteins and Coding Sequences  
NUMBER OF SEQUENCES: 17  
CORRESPONDENCE ADDRESS:  
ADDRESSER: Greenlee and Winner, P.C.  
STREET: 5370 Manhattan Circle, Suite 201

CITY: Boulder  
STATE: Colorado  
COUNTRY: US  
ZIP: 80303

## COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/483,101  
FILING DATE: 07-JUN-1995  
CLASSIFICATION: 424  
ATTORNEY/AGENT INFORMATION:  
NAME: Ferber, Donna M.  
REGISTRATION NUMBER: 33878  
REFERENCE/DOCKET NUMBER: 6-95  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (303) 499-8080  
TELEFAX: (303) 499-8089  
INFORMATION FOR SEQ ID NO: 11:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 170 amino acids  
TYPE: amino acid  
STRANDEDNESS:  
TOPOLOGY: unknown  
MOLECULE TYPE: protein  
HYPOTHETICAL: NO  
US-08-483-101-11

Query Match 100.0%; Score 68; DB 2; Length 170;

Best Local Similarity 100.0%; Pred. No. 0.00014;  
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KTAGTAPTAGNYS 13  
Db 147 KTAGTAPTAGNYS 159

## RESULT 4

US-09-252-991A-30331  
Sequence 30331, Application US/09252991A  
Patent No. 6551795  
GENERAL INFORMATION:  
APPLICANT: Marc J. Rubenfield et al.  
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS  
TITLE OF INVENTION: AERGINOSA FOR DIAGNOSTICS AND THERAPEUTICS  
FILE REFERENCE: 107196.136  
CURRENT APPLICATION NUMBER: US/09/252,991A  
CURRENT FILING DATE: 1999-02-18  
PRIOR APPLICATION NUMBER: US 60/074,788  
PRIOR FILING DATE: 1998-02-18  
PRIOR APPLICATION NUMBER: US 60/094,190  
PRIOR FILING DATE: 1998-07-27  
NUMBER OF SEQ ID NOS: 33142  
SEQ ID NO 30331  
LENGTH: 175  
TYPE: PRT  
ORGANISM: Pseudomonas aeruginosa  
US-09-252-991A-30331

Query Match 57.4%; Score 39; DB 4; Length 175;

Best Local Similarity 61.5%; Pred. No. 17;  
Matches 8; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 1 KTAGTAPTAGNYS 13  
Db 111 RTAGTPTARSS 123

## RESULT 5

US-09-056-556-202  
Sequence 202, Application US/09056556



Patent No. 6350456  
GENERAL INFORMATION:  
APPLICANT: Reed, Steven G.  
APPLICANT: Skeiky, Yasir A.W.  
APPLICANT: Dillon, David C.  
TITLE OF INVENTION: COMPOUNDS AND METHODS FOR THE PREVENTION AND  
NUMBER OF SEQUENCES: 241  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: SEED AND BERRY LLP  
STREET: 6300 Columbia Center, 701 Fifth Avenue  
City: Seattle  
STATE: Washington  
COUNTRY: USA  
ZIP: 98104-7092  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/056,556  
FILING DATE: 07-APR-1998  
CLASSIFICATION:  
ATTORNEY/AGENT INFORMATION:  
NAME: Makl, David J.  
REGISTRATION NUMBER: 31,392  
REFERENCE/DOCKET NUMBER: 210121.457  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (206) 622-4900  
TELEFAX: (206) 682-6031  
INFORMATION FOR SEQ ID NO: 202:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 376 amino acids  
TYPE: amino acid  
STRANDEDNESS:  
TOPOLOGY: linear  
US-09-056-556-202

Query Match 57.4%; Score 39; DB 4; Length 376;  
Best Local Similarity 63.6%; Pred. No. 41;  
Matches 7; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 3 AGTAPTAGNYS 13  
Db 51 AATTPTAGYT 61

RESULT 6  
US-09-072-596-197  
Sequence 197, Application US/09072596  
Patent No. 6458366  
GENERAL INFORMATION:  
APPLICANT: Reed, Steven G.  
APPLICANT: Skeiky, Yasir A.W.  
APPLICANT: Dillon, David C.  
APPLICANT: Campos-Nevo, Antonia  
APPLICANT: Houghton, Raymond  
APPLICANT: Veditz, Thomas S.  
APPLICANT: Twardzik, Daniel R.  
APPLICANT: Lodes, Michael J.  
APPLICANT: Hendrickson, Ronald C.  
TITLE OF INVENTION: COMPOUNDS AND METHODS FOR DIAGNOSIS OF  
NUMBER OF SEQUENCES: 350  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: SEED AND BERRY LLP  
STREET: 6300 Columbia Center, 701 Fifth Avenue  
City: Seattle  
STATE: Washington  
COUNTRY: USA  
ZIP: 98104-7092  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/072,596  
FILING DATE: 05-MAY-1998  
CLASSIFICATION:  
ATTORNEY/AGENT INFORMATION:  
NAME: Makl, David J.  
REGISTRATION NUMBER: 31,392  
REFERENCE/DOCKET NUMBER: 210121.417C9  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (206) 622-4900  
TELEFAX: (206) 682-6031  
INFORMATION FOR SEQ ID NO: 197:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 376 amino acids  
TYPE: amino acid  
STRANDEDNESS:  
TOPOLOGY: linear  
US-09-072-596-197

Query Match 57.4%; Score 39; DB 4; Length 376;  
Best Local Similarity 63.6%; Pred. No. 41;  
Matches 7; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 3 AGTAPTAGNYS 13  
Db 51 AATTPTAGYT 61

RESULT 7  
US-09-252-991A-26586  
Sequence 26586, Application US/09252991A  
Patent No. 6551795  
GENERAL INFORMATION:  
APPLICANT: Marc J. Rubenfield et al.  
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS  
FILE REFERENCE: 107196.136  
CURRENT APPLICATION NUMBER: US/09/252,991A  
CURRENT FILING DATE: 1999-02-18  
PRIOR APPLICATION NUMBER: US 60/074,788  
PRIOR FILING DATE: 1998-02-18  
PRIOR APPLICATION NUMBER: US 60/094,190  
PRIOR FILING DATE: 1998-07-27  
NUMBER OF SEQ ID NOS: 33142  
SEQ ID NO 26586  
LENGTH: 328  
TYPE: PRT  
ORGANISM: Pseudomonas aeruginosa  
US-09-252-991A-26586

Query Match 55.9%; Score 38; DB 4; Length 328;  
Best Local Similarity 63.6%; Pred. No. 53;  
Matches 7; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 3 AGTAPTAGNYS 13  
Db 80 ASSAPVAGSY 90

RESULT 8  
US-09-173-300-20  
Sequence 20, Application US/09173300  
Patent No. 6451581  
GENERAL INFORMATION:  
APPLICANT: Falco, Saverio Carl  
APPLICANT: Hitz, William D.  
APPLICANT: Kinney, Anthony J.  
APPLICANT: Cahoon, Rebecca E.  
APPLICANT: Rafalski, J. Antoni  
TITLE OF INVENTION: PLANT BRANCHED CHAIN AMINO ACID BIOSYNTHETIC  
FILE REFERENCE: BB-1126

; CURRENT APPLICATION NUMBER: US/09/173,300  
 ; CURRENT FILING DATE: 1998-10-15  
 ; EARLIER APPLICATION NUMBER: 60/063,423  
 ; EARLIER FILING DATE: 1997 October 28  
 ; NUMBER OF SEQ ID NOS: 54  
 ; SOFTWARE: Microsoft Word Version 7.0A  
 ; SEQ ID NO 20  
 ; LENGTH: 363  
 ; TYPE: PRT  
 ; ORGANISM: Bacillus subtilis  
 US-09-173-300-20

Query Match 55.9%; Score 38; DB 4; Length 363;  
 Best Local Similarity 70.0%; Pred. No. 59;  
 Matches 7; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 4 GTAPTAGNYS 13  
 DB 194 GNAKTAGNYA 203

RESULT 9  
 US-09-252-991A-32936  
 ; Sequence 32936, Application US/09252991A  
 ; Patent No. 6551795  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Marc J. Rubenfield et al.  
 ; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS  
 ; FILE REFERENCE: 107196.136  
 ; CURRENT APPLICATION NUMBER: US/09/252,991A  
 ; CURRENT FILING DATE: 1999-02-18  
 ; PRIOR APPLICATION NUMBER: US 60/074,788  
 ; PRIOR FILING DATE: 1998-02-18  
 ; PRIOR APPLICATION NUMBER: US 60/094,190  
 ; PRIOR FILING DATE: 1998-07-27  
 ; NUMBER OF SEQ ID NOS: 33142  
 ; SEQ ID NO 32936  
 ; LENGTH: 501  
 ; TYPE: PRT  
 ; ORGANISM: Pseudomonas aeruginosa  
 US-09-252-991A-32936

Query Match 55.9%; Score 38; DB 4; Length 501;  
 Best Local Similarity 77.8%; Pred. No. 87;  
 Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 2 TAGTAPTAG 10  
 DB 227 TAGSCTAG 235

RESULT 10  
 US-08-760-615-2  
 ; Sequence 2, Application US/08760615  
 ; Patent No. 6200959  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Haynes, Joel R  
 ; APPLICANT: Schmaljohn, Connie S  
 ; APPLICANT: Fuller, Deborah L  
 ; APPLICANT: Schmaljohn, Alan  
 ; APPLICANT: Jahrling, Peter B  
 ; TITLE OF INVENTION: GENETIC INDUCTION OF ANTI-VIRAL IMMUNE  
 ; TITLE OF INVENTION: RESPONSE AND GENETIC VACCINE FOR FILOVIRUS  
 ; NUMBER OF SEQUENCES: 17  
 ; CORRESPONDENCE ADDRESSES:  
 ; ADDRESS: Charles & Brady  
 ; STREET: 1 South Pinckney Street  
 ; CITY: Madison  
 ; STATE: WI  
 ; COUNTRY: US  
 ; ZIP: 53703

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk  
 ; COMPUTER: IBM PC compatible  
 ; OPERATING SYSTEM: PC-DOS/MS-DOS  
 ; SOFTWARE: Patentin Release #1.0, Version #1.30  
 ; CURRENT APPLICATION DATA:  
 ; APPLICATION NUMBER: US/08/760,615  
 ; FILING DATE:  
 ; CLASSIFICATION: 435  
 ; ATTORNEY/AGENT INFORMATION:  
 ; NAME: Berson, Bennett J  
 ; REGISTRATION NUMBER: 37094  
 ; REFERENCE/DOCKET NUMBER: 110229.91241  
 ; TELECOMMUNICATION INFORMATION:  
 ; TELEPHONE: 608-251-5000  
 ; TELEFAX: 608-251-9166  
 ; INFORMATION FOR SEQ ID NO: 2:  
 ; SEQUENCE CHARACTERISTICS:  
 ; LENGTH: 676 amino acids  
 ; TYPE: amino acid  
 ; TOPOLOGY: linear  
 ; MOLECULE TYPE: protein  
 US-08-760-615-2

Query Match 55.9%; Score 38; DB 3; Length 676;  
 Best Local Similarity 46.2%; Pred. No. 1,2e+02;  
 Matches 6; Conservative 4; Mismatches 3; Indels 0; Gaps 0;

QY 1 KTAGTAPTAGNYS 13  
 DB 140 KVSCTGCPAGDPA 152

RESULT 11  
 US-09-252-991A-30797  
 ; Sequence 30797, Application US/09252991A  
 ; Patent No. 6551795  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Marc J. Rubenfield et al.  
 ; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS  
 ; FILE REFERENCE: 107196.136  
 ; CURRENT APPLICATION NUMBER: US/09/252,991A  
 ; CURRENT FILING DATE: 1999-02-18  
 ; PRIOR APPLICATION NUMBER: US 60/074,788  
 ; PRIOR FILING DATE: 1998-02-18  
 ; PRIOR APPLICATION NUMBER: US 60/094,190  
 ; PRIOR FILING DATE: 1998-07-27  
 ; NUMBER OF SEQ ID NOS: 33142  
 ; SEQ ID NO 30797  
 ; LENGTH: 311  
 ; TYPE: PRT  
 ; ORGANISM: Pseudomonas aeruginosa  
 US-09-252-991A-30797

Query Match 54.4%; Score 37; DB 4; Length 311;  
 Best Local Similarity 66.7%; Pred. No. 74;  
 Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 4 GTAPTAGNY 12  
 DB 293 GSLPSAGNY 301

RESULT 12  
 US-08-818-112-69  
 ; Sequence 69, Application US/08818112  
 ; Patent No. 6290969  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Reed, Steven G.  
 ; APPLICANT: Skeiky, Yasir A.W.  
 ; APPLICANT: Dillon, Davin C.  
 ; APPLICANT: Campos-Neto, Antonio  
 ; APPLICANT: Houghton, Raymond

; COMPUTER READABLE FORM:

APPLICANT: Vedick, Thomas S.  
APPLICANT: Twardzik, Daniel R.  
TITLE OF INVENTION: COMPOUNDS AND METHODS FOR IMMUNOTHERAPY  
TITLE OF INVENTION: AND DIAGNOSIS OF TUBERCULOSIS  
NUMBER OF SEQUENCES: 153  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: SEED AND BERRY LLP  
STREET: 6300 Columbia Center, 701 Fifth Avenue  
CITY: Seattle  
STATE: Washington  
COUNTRY: USA  
ZIP: 98104-7092  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/818,112  
FILING DATE: 13-MAR-1997  
CLASSIFICATION: 424  
ATTORNEY/AGENT INFORMATION:  
NAME: Maki, David J.  
REGISTRATION NUMBER: 31,392  
REFERENCE/DOCKET NUMBER: 210121.411C6  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (206) 622-4900  
TELEFAX: (206) 682-6031  
INFORMATION FOR SEQ ID NO: 69:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 344 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
US-08-818-112-69

Query Match 54.4%; Score 37; DB 3; Length 344;  
Best Local Similarity 77.8%; Pred. No. 84;  
Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 3 AGTAPTAGN 11  
Db 106 AGTAPTAGD 114

RESULT 13  
US-08-818-111-70  
Sequence 70, Application US/08818111  
Patent No. 6338852  
GENERAL INFORMATION:  
APPLICANT: Reed, Steven G.  
APPLICANT: Skeiky, Yasir A.W.  
APPLICANT: Dillon, David J.  
APPLICANT: Campos-Neto, Antonia  
APPLICANT: Houghton, Raymond  
APPLICANT: Vedick, Thomas S.  
APPLICANT: Twardzik, Daniel R.  
TITLE OF INVENTION: COMPOUNDS AND METHODS FOR DIAGNOSIS OF  
NUMBER OF SEQUENCES: 148  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: SEED AND BERRY LLP  
STREET: 6300 Columbia Center, 701 Fifth Avenue  
CITY: Seattle  
STATE: Washington  
COUNTRY: USA  
ZIP: 98104-7092  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/818,111

FILING DATE: 13-MAR-1997  
CLASSIFICATION: 424  
ATTORNEY/AGENT INFORMATION:  
NAME: Maki, David J.  
REGISTRATION NUMBER: 31,392  
REFERENCE/DOCKET NUMBER: 210121.417C6  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (206) 622-4900  
TELEFAX: (206) 682-6031  
INFORMATION FOR SEQ ID NO: 70:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 344 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
US-08-818-111-70

Query Match 54.4%; Score 37; DB 4; Length 344;  
Best Local Similarity 77.8%; Pred. No. 84;  
Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 3 AGTAPTAGN 11  
Db 106 AGTAPTAGD 114

RESULT 14  
US-09-056-556-69  
Sequence 69, Application US/09056556  
Patent No. 6350456  
GENERAL INFORMATION:  
APPLICANT: Reed, Steven G.  
APPLICANT: Skeiky, Yasir A.W.  
APPLICANT: Dillon, David J.  
TITLE OF INVENTION: COMPOUNDS AND METHODS FOR THE PREVENTION AND  
NUMBER OF SEQUENCES: 241  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: SEED AND BERRY LLP  
STREET: 6300 Columbia Center, 701 Fifth Avenue  
CITY: Seattle  
STATE: Washington  
COUNTRY: USA  
ZIP: 98104-7092  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/056,556  
FILING DATE: 07-APR-1998  
CLASSIFICATION:  
ATTORNEY/AGENT INFORMATION:  
NAME: Maki, David J.  
REGISTRATION NUMBER: 31,392  
REFERENCE/DOCKET NUMBER: 210121.457  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (206) 622-4900  
TELEFAX: (206) 682-6031  
INFORMATION FOR SEQ ID NO: 69:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 344 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
US-09-056-556-69

Query Match 54.4%; Score 37; DB 4; Length 344;  
Best Local Similarity 77.8%; Pred. No. 84;  
Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 3 AGTAPTAGN 11  
Db 106 AGTAPTAGD 114

Db 106 AGTAPAGD 114

## RESULT 15

US-09-072-596-70

; Sequence 70, Application US/09072596

; Patent No. 6458366

; GENERAL INFORMATION:

; APPLICANT: Reed, Steven G.

; APPLICANT: Skeiky, Yasir A.W.

; APPLICANT: Dillon, Davin C.

; APPLICANT: Campos-Neto, Antonia

; APPLICANT: Houghton, Raymond

; APPLICANT: Vedvick, Thomas S.

; APPLICANT: Twardzik, Daniel R.

; APPLICANT: Lodes, Michael J.

; APPLICANT: Hendrickson, Ronald C.

; TITLE OF INVENTION: COMPOUNDS AND METHODS FOR DIAGNOSIS OF

; NUMBER OF SEQUENCES: 350 TUBERCULOSIS

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: SEED and BERRY LLP

; STREET: 6300 Columbia Center, 701 Fifth Avenue

; CITY: Seattle

; STATE: Washington

; COUNTRY: USA

; ZIP: 98104-7092

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: Patentin Release #1.0, Version #1.30

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/09/072,596

; FILING DATE: 05-MAY-1998

; CLASSIFICATION:

; ATTORNEY/AGENT INFORMATION:

; NAME: Makl, David J.

; REGISTRATION NUMBER: 31,392

; REFERENCE/DOCKET NUMBER: 210121.417C9

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: (206) 622-4900

; TELEFAX: (206) 682-6031

; INFORMATION FOR SEQ ID NO: 70:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 344 amino acids

; TYPE: amino acid

; STRANDEDNESS: single

; TOPOLOGY: linear

; US-09-072-596-70

; Query Match 54.4%; Score 37; DB 4; Length 344;

; Best Local Similarity 77.8%; Pred. No. 84;

; Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

; QY 3 AGTAPTAGN 11

; DB 106 AGTAPAGD 114

; Search completed: February 6, 2004, 11:40:46

; Job time : 22 secs

GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: February 6, 2004, 11:39:31 ; Search time 34 Seconds  
(without alignments)  
80.058 Million cell updates/sec

Title: US-09-618-577-28  
Perfect score: 68  
Sequence: 1 KTAGTAPTAGNYS 13

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 801455 seqs, 209382283 residues  
Total number of hits satisfying chosen parameters: 801455

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

Published Applications\_AA:\*

- 1: /cgn2\_6/ptodata/1/pubpaa/US07\_PUBCOMB.pep:\*
- 2: /cgn2\_6/ptodata/1/pubpaa/PC7\_NEW\_PUB.pep:\*
- 3: /cgn2\_6/ptodata/1/pubpaa/US06\_NEW\_PUB.pep:\*
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- 5: /cgn2\_6/ptodata/1/pubpaa/US07\_NEW\_PUB.pep:\*
- 6: /cgn2\_6/ptodata/1/pubpaa/PC7US\_PUBCOMB.pep:\*
- 7: /cgn2\_6/ptodata/1/pubpaa/US08\_NEW\_PUB.pep:\*
- 8: /cgn2\_6/ptodata/1/pubpaa/US08\_PUBCOMB.pep:\*
- 9: /cgn2\_6/ptodata/1/pubpaa/US09\_PUBCOMB.pep:\*
- 10: /cgn2\_6/ptodata/1/pubpaa/US09B\_PUBCOMB.pep:\*
- 11: /cgn2\_6/ptodata/1/pubpaa/US09C\_PUBCOMB.pep:\*
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- 13: /cgn2\_6/ptodata/1/pubpaa/US10A\_PUBCOMB.pep:\*
- 14: /cgn2\_6/ptodata/1/pubpaa/US10B\_PUBCOMB.pep:\*
- 15: /cgn2\_6/ptodata/1/pubpaa/US10C\_PUBCOMB.pep:\*
- 16: /cgn2\_6/ptodata/1/pubpaa/US10\_NEW\_PUB.pep:\*
- 17: /cgn2\_6/ptodata/1/pubpaa/US60\_NEW\_PUB.pep:\*
- 18: /cgn2\_6/ptodata/1/pubpaa/US60\_PUBCOMB.pep:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	68	100.0	13	US-10-224-125-22	Sequence 22, App1
2	68	100.0	147	US-10-224-125-38	Sequence 38, App1
3	68	100.0	147	US-10-224-125-39	Sequence 39, App1
4	68	100.0	147	US-10-224-125-40	Sequence 40, App1
5	68	100.0	168	US-09-839-894-34	Sequence 34, App1
6	58	85.3	11	US-10-224-125-25	Sequence 25, App1
7	54	79.4	10	US-10-224-125-10	Sequence 10, App1
8	54	79.4	10	US-10-224-125-21	Sequence 21, App1
9	48	70.6	134	US-09-839-894-40	Sequence 40, App1
10	46	67.6	167	US-09-839-894-4	Sequence 4, App1
11	42	61.8	980	US-10-369-493-20514	Sequence 38, App1
12	42	61.8	8	US-10-224-125-20	Sequence 20, App1
13	41	60.3	179	US-10-001-245-213	Sequence 213, App1
14	41	60.3	313	US-10-001-245-212	Sequence 212, App1
15	41	60.3	313	US-10-001-245-212	Sequence 212, App1

16	40	58.8	362	12	US-10-374-780A-2098	Sequence 2098, App
17	40	58.8	510	12	US-10-369-493-4244	Sequence 4244, App
18	39	57.4	333	11	US-09-847-208-147	Sequence 147, App
19	39	57.4	333	12	US-10-001-245-189	Sequence 189, App
20	39	57.4	376	12	US-10-084-843-202	Sequence 202, App
21	39	57.4	376	12	US-10-193-002-197	Sequence 197, App
22	38	55.9	297	12	US-10-353-856-15	Sequence 15, App1
23	38	55.9	297	12	US-10-353-856-33	Sequence 33, App1
24	38	55.9	363	14	US-10-027-450-20	Sequence 20, App1
25	38	55.9	364	12	US-10-353-856-14	Sequence 14, App1
26	38	55.9	364	12	US-10-353-856-32	Sequence 32, App1
27	38	55.9	364	12	US-10-353-856-42	Sequence 42, App1
28	38	55.9	464	15	US-10-156-761-10151	Sequence 10151, A
29	38	55.9	676	10	US-09-337-946A-17	Sequence 17, App1
30	38	55.9	676	12	US-10-353-856-13	Sequence 13, App1
31	38	55.9	676	12	US-10-353-856-31	Sequence 31, App1
32	38	55.9	676	12	US-10-353-856-41	Sequence 41, App1
33	38	55.9	676	15	US-10-066-506A-12	Sequence 12, App1
34	38	55.9	747	15	US-10-066-506A-2	Sequence 2, App1
35	38	55.9	1079	11	US-09-820-843A-20	Sequence 20, App1
36	38	55.9	2037	15	US-10-184-644-591	Sequence 591, App
37	38	55.9	2037	15	US-10-184-634-591	Sequence 591, App
38	38	55.9	2700	12	US-10-140-472-27	Sequence 27, App1
39	38	55.9	2700	12	US-10-141-761-27	Sequence 27, App1
40	38	55.9	2700	12	US-10-142-885-27	Sequence 27, App1
41	38	55.9	2700	12	US-10-158-790-27	Sequence 27, App1
42	38	55.9	2700	12	US-10-137-871-27	Sequence 27, App1
43	38	55.9	2700	12	US-10-140-805-27	Sequence 27, App1
44	38	55.9	2700	12	US-10-140-864-27	Sequence 27, App1
45	38	55.9	2700	12	US-10-140-923-27	Sequence 27, App1

#### ALIGNMENTS

RESULT 1  
US-10-224-125-22  
Sequence 22, Application US/10224125  
Publication No. US20030161869A1  
GENERAL INFORMATION:  
APPLICANT: REID, ROBERT H.  
APPLICANT: BOEDERER, EDGAR C.  
APPLICANT: VAN HAMONT, JOHN  
APPLICANT: SETTERSTROM, JEAN A.  
APPLICANT: MCCOEN, CHARLES  
APPLICANT: CASSELS, FREDERICK  
TITLE OF INVENTION: VACCINES AGAINST DISEASES CAUSED BY ENTEROPATHOGENIC  
TITLE OF INVENTION: ORGANISMS USING ANTIGENS ENCAPSULATED WITHIN  
FILE REFERENCE: Army 108  
CURRENT APPLICATION NUMBER: US/10/224,125  
CURRENT FILING DATE: 2002-08-20  
PRIOR APPLICATION NUMBER: 08/789,734  
PRIOR FILING DATE: 1997-01-27  
PRIOR APPLICATION NUMBER: 08/352,944  
PRIOR FILING DATE: 1994-12-09  
PRIOR APPLICATION NUMBER: 08/034,949  
PRIOR FILING DATE: 1993-03-22  
PRIOR APPLICATION NUMBER: 07/867,301  
PRIOR FILING DATE: 1992-04-10  
PRIOR APPLICATION NUMBER: 07/805,721  
PRIOR FILING DATE: 1991-11-21  
PRIOR APPLICATION NUMBER: 07/690,485  
PRIOR FILING DATE: 1991-04-24  
PRIOR APPLICATION NUMBER: 07/521,945  
PRIOR FILING DATE: 1990-05-11  
PRIOR APPLICATION NUMBER: 07/493,597  
PRIOR FILING DATE: 1990-03-15  
PRIOR APPLICATION NUMBER: 06/590,308  
PRIOR FILING DATE: 1984-03-16  
NUMBER OF SEQ ID NOS: 40  
SOFTWARE: PatentIn Ver. 2.1  
SEQ ID NO 22

LENGTH: 13  
TYPE: PRT  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: Description of Artificial Sequence: Synthetic  
US-10-224-125-22

Query Match 100.0%; Score 68; DB 12; Length 13;  
Best Local Similarity 100.0%; Pred. No. 7.2e-05;  
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KTAGTAPTAGNYS 13  
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Db 1 KTAGTAPTAGNYS 13

RESULT 2  
US-10-224-125-38

Sequence 38, Application US/10224125  
Publication No. US20030161889A1  
GENERAL INFORMATION:

APPLICANT: REID, ROBERT H.  
APPLICANT: BOEDEKER, EDGAR C.  
APPLICANT: VAN HAMONT, JOHN  
APPLICANT: SETTERSTROM, JEAN A.  
APPLICANT: MCOUEN, CHARLES  
APPLICANT: CASSELS, FREDERICK  
TITLE OF INVENTION: VACCINES AGAINST DISEASES CAUSED BY ENTEROPATHOGENIC  
TITLE OF INVENTION: ORGANISMS USING ANTIGENS ENCAPSULATED WITHIN  
FILE REFERENCE: Army 108  
CURRENT APPLICATION NUMBER: US/10/224,125  
CURRENT FILING DATE: 2002-08-20

PRIOR APPLICATION NUMBER: 08/789,734  
PRIOR FILING DATE: 1997-01-27  
PRIOR APPLICATION NUMBER: 08/352,944  
PRIOR FILING DATE: 1994-12-09  
PRIOR APPLICATION NUMBER: 08/034,949  
PRIOR FILING DATE: 1993-03-22  
PRIOR APPLICATION NUMBER: 07/867,301  
PRIOR FILING DATE: 1992-04-10  
PRIOR APPLICATION NUMBER: 07/805,721  
PRIOR FILING DATE: 1991-11-21  
PRIOR APPLICATION NUMBER: 07/690,485  
PRIOR FILING DATE: 1991-04-24  
PRIOR APPLICATION NUMBER: 07/521,945  
PRIOR FILING DATE: 1990-05-11  
PRIOR APPLICATION NUMBER: 07/493,597  
PRIOR FILING DATE: 1990-03-15  
PRIOR APPLICATION NUMBER: 06/590,308  
PRIOR FILING DATE: 1984-03-16  
NUMBER OF SEQ ID NOS: 40  
SOFTWARE: PatentIn Ver. 2.1  
SEQ ID NO 38  
LENGTH: 147  
TYPE: PRT  
ORGANISM: Macaca mulatta  
US-10-224-125-38

Query Match 100.0%; Score 68; DB 12; Length 147;  
Best Local Similarity 100.0%; Pred. No. 0.00094;  
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KTAGTAPTAGNYS 13  
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Db 124 KTAGTAPTAGNYS 136

RESULT 3

US-10-224-125-39  
Sequence 39, Application US/10224125  
Publication No. US20030161889A1

GENERAL INFORMATION:  
APPLICANT: REID, ROBERT H.  
APPLICANT: BOEDEKER, EDGAR C.  
APPLICANT: VAN HAMONT, JOHN  
APPLICANT: SETTERSTROM, JEAN A.  
APPLICANT: MCOUEN, CHARLES  
APPLICANT: CASSELS, FREDERICK  
TITLE OF INVENTION: VACCINES AGAINST DISEASES CAUSED BY ENTEROPATHOGENIC  
TITLE OF INVENTION: ORGANISMS USING ANTIGENS ENCAPSULATED WITHIN  
FILE REFERENCE: Army 108  
CURRENT APPLICATION NUMBER: US/10/224,125  
CURRENT FILING DATE: 2002-08-20

PRIOR APPLICATION NUMBER: 08/789,734  
PRIOR FILING DATE: 1997-01-27  
PRIOR APPLICATION NUMBER: 08/352,944  
PRIOR FILING DATE: 1994-12-09  
PRIOR APPLICATION NUMBER: 08/034,949  
PRIOR FILING DATE: 1993-03-22  
PRIOR APPLICATION NUMBER: 07/867,301  
PRIOR FILING DATE: 1992-04-10  
PRIOR APPLICATION NUMBER: 07/805,721  
PRIOR FILING DATE: 1991-11-21  
PRIOR APPLICATION NUMBER: 07/690,485  
PRIOR FILING DATE: 1991-04-24  
PRIOR APPLICATION NUMBER: 07/521,945  
PRIOR FILING DATE: 1990-05-11  
PRIOR APPLICATION NUMBER: 07/493,597  
PRIOR FILING DATE: 1990-03-15  
PRIOR APPLICATION NUMBER: 06/590,308  
PRIOR FILING DATE: 1984-03-16  
NUMBER OF SEQ ID NOS: 40  
SOFTWARE: PatentIn Ver. 2.1  
SEQ ID NO 39  
LENGTH: 147  
TYPE: PRT  
ORGANISM: Macaca mulatta  
US-10-224-125-39

Query Match 100.0%; Score 68; DB 12; Length 147;  
Best Local Similarity 100.0%; Pred. No. 0.00094;  
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KTAGTAPTAGNYS 13  
|||||  
Db 124 KTAGTAPTAGNYS 136

RESULT 4  
US-10-224-125-40

Sequence 40, Application US/10224125  
Publication No. US20030161889A1  
GENERAL INFORMATION:

APPLICANT: REID, ROBERT H.  
APPLICANT: BOEDEKER, EDGAR C.  
APPLICANT: VAN HAMONT, JOHN  
APPLICANT: SETTERSTROM, JEAN A.  
APPLICANT: MCOUEN, CHARLES  
APPLICANT: CASSELS, FREDERICK  
TITLE OF INVENTION: VACCINES AGAINST DISEASES CAUSED BY ENTEROPATHOGENIC  
TITLE OF INVENTION: ORGANISMS USING ANTIGENS ENCAPSULATED WITHIN  
FILE REFERENCE: Army 108  
CURRENT APPLICATION NUMBER: US/10/224,125  
CURRENT FILING DATE: 2002-08-20  
PRIOR APPLICATION NUMBER: 08/789,734  
PRIOR FILING DATE: 1997-01-27  
PRIOR APPLICATION NUMBER: 08/352,944  
PRIOR FILING DATE: 1994-12-09  
PRIOR APPLICATION NUMBER: 08/034,949  
PRIOR FILING DATE: 1993-03-22  
PRIOR APPLICATION NUMBER: 07/867,301  
PRIOR FILING DATE: 1992-04-10

;; PRIOR APPLICATION NUMBER: 07/805,721  
;; PRIOR FILING DATE: 1991-11-21  
;; PRIOR APPLICATION NUMBER: 07/690,485  
;; PRIOR FILING DATE: 1991-04-24  
;; PRIOR APPLICATION NUMBER: 07/521,945  
;; PRIOR FILING DATE: 1990-05-11  
;; PRIOR APPLICATION NUMBER: 07/493,597  
;; PRIOR FILING DATE: 1990-03-15  
;; PRIOR APPLICATION NUMBER: 06/590,308  
;; PRIOR FILING DATE: 1984-03-16  
;; NUMBER OF SEQ ID NOS: 40  
;; SOFTWARE: Patentln Ver. 2.1  
;; SEQ ID NO 40  
;; LENGTH: 147  
;; TYPE: PRT  
;; ORGANISM: Macaca mulatta  
US-10-224-125-40

Query Match 100.0%; Score 68; DB 12; Length 147;  
Best Local Similarity 100.0%; Pred. No. 0.00094;  
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KTACTAPTAGNYS 13  
DB 124 KTACTAPTAGNYS 136

RESULT 5  
US-09-839-894-34  
;; Sequence 34, Application US/09839894  
;; Patent No. US20020176868A1  
;; GENERAL INFORMATION:  
;; APPLICANT: Alldoun, Zeev  
;; APPLICANT: Barry, Eileen M.  
;; APPLICANT: Levine, Myron M.  
;; APPLICANT: University of Maryland  
;; TITLE OF INVENTION: ISOLATION AND CHARACTERIZATION OF THE  
;; TITLE OF INVENTION: CSA OPERON  
;; FILE REFERENCE: UOFMD.006A  
;; CURRENT APPLICATION NUMBER: US/09/839,894  
;; CURRENT FILING DATE: 2001-04-20  
;; PRIOR APPLICATION NUMBER: 60/198,626  
;; PRIOR FILING DATE: 2000-04-20  
;; NUMBER OF SEQ ID NOS: 40  
;; SOFTWARE: FastSeq for Windows Version 4.0  
;; SEQ ID NO 34  
;; LENGTH: 168  
;; TYPE: PRT  
;; ORGANISM: Artificial Sequence  
;; FEATURE:  
;; OTHER INFORMATION: ETEC Protein Homology Sequence  
US-09-839-894-34

Query Match 100.0%; Score 68; DB 10; Length 168;  
Best Local Similarity 100.0%; Pred. No. 0.0011;  
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KTACTAPTAGNYS 13  
DB 145 KTACTAPTAGNYS 157

RESULT 6  
US-10-224-125-25  
;; Sequence 25, Application US/10224125  
;; Publication No. US20030161889A1  
;; GENERAL INFORMATION:  
;; APPLICANT: REID, ROBERT H.  
;; APPLICANT: BOEDEKER, EDGAR C.  
;; APPLICANT: VAN HAMONT, JOHN  
;; APPLICANT: SETTERSTROM, JEAN A.  
;; APPLICANT: MCOUEEN, CHARLES  
;; APPLICANT: CASSELS, FREDERICK

;; TITLE OF INVENTION: VACCINES AGAINST DISEASES CAUSED BY ENTEROPATHOGENIC  
;; TITLE OF INVENTION: ORGANISMS USING ANTIGENS ENCAPSULATED WITHIN  
;; TITLE OF INVENTION: BIODEGRADABLE-BIODEGRADABLE MICROSPHERES  
;; FILE REFERENCE: Army 108  
;; CURRENT APPLICATION NUMBER: US/10/224,125  
;; CURRENT FILING DATE: 2002-08-20  
;; PRIOR APPLICATION NUMBER: 08/789,734  
;; PRIOR FILING DATE: 1997-01-27  
;; PRIOR APPLICATION NUMBER: 08/352,944  
;; PRIOR FILING DATE: 1994-12-09  
;; PRIOR APPLICATION NUMBER: 08/034,949  
;; PRIOR FILING DATE: 1993-03-22  
;; PRIOR APPLICATION NUMBER: 07/867,301  
;; PRIOR FILING DATE: 1992-04-10  
;; PRIOR APPLICATION NUMBER: 07/805,721  
;; PRIOR FILING DATE: 1991-11-21  
;; PRIOR APPLICATION NUMBER: 07/690,485  
;; PRIOR FILING DATE: 1991-04-24  
;; PRIOR APPLICATION NUMBER: 07/521,945  
;; PRIOR FILING DATE: 1990-05-11  
;; PRIOR APPLICATION NUMBER: 07/493,597  
;; PRIOR FILING DATE: 1990-03-15  
;; PRIOR APPLICATION NUMBER: 06/590,308  
;; PRIOR FILING DATE: 1984-03-16  
;; NUMBER OF SEQ ID NOS: 40  
;; SOFTWARE: Patentln Ver. 2.1  
;; SEQ ID NO 25  
;; LENGTH: 11  
;; TYPE: PRT  
;; ORGANISM: Artificial Sequence  
;; FEATURE:  
;; OTHER INFORMATION: Description of Artificial Sequence: Synthetic  
US-10-224-125-25

Query Match 85.3%; Score 58; DB 12; Length 11;  
Best Local Similarity 100.0%; Pred. No. 0.0028;  
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 AGTAPTAGNYS 13  
DB 1 AGTAPTAGNYS 11

RESULT 7  
US-10-224-125-10  
;; Sequence 10, Application US/10224125  
;; Publication No. US20030161889A1  
;; GENERAL INFORMATION:  
;; APPLICANT: REID, ROBERT H.  
;; APPLICANT: BOEDEKER, EDGAR C.  
;; APPLICANT: VAN HAMONT, JOHN  
;; APPLICANT: SETTERSTROM, JEAN A.  
;; APPLICANT: MCOUEEN, CHARLES  
;; APPLICANT: CASSELS, FREDERICK  
;; TITLE OF INVENTION: VACCINES AGAINST DISEASES CAUSED BY ENTEROPATHOGENIC  
;; TITLE OF INVENTION: ORGANISMS USING ANTIGENS ENCAPSULATED WITHIN  
;; TITLE OF INVENTION: BIODEGRADABLE-BIODEGRADABLE MICROSPHERES  
;; FILE REFERENCE: Army 108  
;; CURRENT APPLICATION NUMBER: US/10/224,125  
;; CURRENT FILING DATE: 2002-08-20  
;; PRIOR APPLICATION NUMBER: 08/789,734  
;; PRIOR FILING DATE: 1997-01-27  
;; PRIOR APPLICATION NUMBER: 08/352,944  
;; PRIOR FILING DATE: 1994-12-09  
;; PRIOR APPLICATION NUMBER: 08/034,949  
;; PRIOR FILING DATE: 1993-03-22  
;; PRIOR APPLICATION NUMBER: 07/867,301  
;; PRIOR FILING DATE: 1992-04-10  
;; PRIOR APPLICATION NUMBER: 07/805,721  
;; PRIOR FILING DATE: 1991-11-21  
;; PRIOR APPLICATION NUMBER: 07/690,485  
;; PRIOR FILING DATE: 1991-04-24

PRIOR APPLICATION NUMBER: 07/521,945  
PRIOR FILING DATE: 1990-05-11  
PRIOR APPLICATION NUMBER: 07/493,597  
PRIOR FILING DATE: 1990-03-15  
PRIOR APPLICATION NUMBER: 06/590,308  
PRIOR FILING DATE: 1984-03-16  
NUMBER OF SEQ ID NOS: 40  
SOFTWARE: Patentin Ver. 2.1  
SEQ ID NO: 10  
LENGTH: 10  
TYPE: PRT  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: Description of Artificial Sequence: Synthetic  
US-10-224-125-10

Query Match 79.4%; Score 54; DB 12; Length 10;  
Best Local Similarity 100.0%; Pred. No. 0.012;  
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 AGTAPTAGNY 12  
Db 1 AGTAPTAGNY 10

RESULT 8  
US-10-224-125-21  
Sequence 21, Application US/107224125  
Publication No. US20030161869A1  
GENERAL INFORMATION:  
APPLICANT: REID, ROBERT H.  
APPLICANT: BOEDEKER, EDGAR C.  
APPLICANT: VAN HAMONT, JOHN  
APPLICANT: SETTERSTROM, JEAN A.  
APPLICANT: MCOHEN, CHARLES  
APPLICANT: CASSIDY, FREDERICK  
TITLE OF INVENTION: VACCINES AGAINST DISEASES CAUSED BY ENTEROPATHOGENIC  
TITLE OF INVENTION: ORGANISMS USING ANTIGENS ENCAPSULATED WITHIN  
FILE REFERENCE: Army 108  
CURRENT APPLICATION NUMBER: US/10/224,125  
CURRENT FILING DATE: 2002-08-20  
PRIOR APPLICATION NUMBER: 08/789,734  
PRIOR FILING DATE: 1997-01-27  
PRIOR APPLICATION NUMBER: 08/352,944  
PRIOR FILING DATE: 1994-12-09  
PRIOR APPLICATION NUMBER: 08/034,949  
PRIOR FILING DATE: 1993-03-22  
PRIOR APPLICATION NUMBER: 07/867,301  
PRIOR FILING DATE: 1992-04-10  
PRIOR APPLICATION NUMBER: 07/805,721  
PRIOR FILING DATE: 1991-11-21  
PRIOR APPLICATION NUMBER: 07/690,485  
PRIOR FILING DATE: 1991-04-24  
PRIOR APPLICATION NUMBER: 07/521,945  
PRIOR FILING DATE: 1990-05-11  
PRIOR APPLICATION NUMBER: 07/493,597  
PRIOR FILING DATE: 1990-03-15  
PRIOR APPLICATION NUMBER: 06/590,308  
PRIOR FILING DATE: 1984-03-16  
NUMBER OF SEQ ID NOS: 40  
SOFTWARE: Patentin Ver. 2.1  
SEQ ID NO: 21  
LENGTH: 10  
TYPE: PRT  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: Description of Artificial Sequence: Synthetic  
US-10-224-125-21

Query Match 79.4%; Score 54; DB 12; Length 10;

Best Local Similarity 100.0%; Pred. No. 0.012;  
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 GTAPTAGNYS 13  
Db 1 GTAPTAGNYS 10

RESULT 9  
US-09-839-894-40  
Sequence 40, Application US/09839894  
Patent No. US20020176868A1  
GENERAL INFORMATION:  
APPLICANT: Altboum, Zeev  
APPLICANT: Barry, Eileen M.  
APPLICANT: Levine, Myron M.  
APPLICANT: University of Maryland  
TITLE OF INVENTION: ISOLATION AND CHARACTERIZATION OF THE  
FILE REFERENCE: CSA OPERON  
CURRENT APPLICATION NUMBER: US/09/839,894  
CURRENT FILING DATE: 2001-04-20  
PRIOR APPLICATION NUMBER: 60/198,626  
PRIOR FILING DATE: 2000-04-20  
NUMBER OF SEQ ID NOS: 40  
SOFTWARE: FastSeq for Windows Version 4.0  
SEQ ID NO: 40  
LENGTH: 134  
TYPE: PRT  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: ETEC Protein Homology Sequence  
US-09-839-894-40

Query Match 70.6%; Score 48; DB 10; Length 134;  
Best Local Similarity 81.8%; Pred. No. 1.8;  
Matches 9; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 2 TAGTAPTAGNY 12  
Db 112 TAGTAPTAGNY 122

RESULT 10  
US-09-839-894-4  
Sequence 4, Application US/09839894  
Patent No. US20020176868A1  
GENERAL INFORMATION:  
APPLICANT: Altboum, Zeev  
APPLICANT: Barry, Eileen M.  
APPLICANT: Levine, Myron M.  
APPLICANT: University of Maryland  
TITLE OF INVENTION: ISOLATION AND CHARACTERIZATION OF THE  
FILE REFERENCE: UOPMD.006A  
CURRENT APPLICATION NUMBER: US/09/839,894  
CURRENT FILING DATE: 2001-04-20  
PRIOR APPLICATION NUMBER: 60/198,626  
PRIOR FILING DATE: 2000-04-20  
NUMBER OF SEQ ID NOS: 40  
SOFTWARE: FastSeq for Windows Version 4.0  
SEQ ID NO: 4  
LENGTH: 167  
TYPE: PRT  
ORGANISM: E. coli  
US-09-839-894-4

Query Match 69.1%; Score 47; DB 10; Length 167;  
Best Local Similarity 75.0%; Pred. No. 3.3;  
Matches 9; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 2 TAGTAPTAGNYS 13



Db 145 TTAQAPTANYS 156

## RESULT 11

US-09-839-894-38  
; Sequence 38, Application US/09839894  
; Patent No. US20020176868A1  
; GENERAL INFORMATION:  
; APPLICANT: Alboum, Zeev  
; APPLICANT: Barry, Eileen M.  
; APPLICANT: Levine, Myron M.  
; APPLICANT: University of Maryland  
; TITLE OF INVENTION: ISOLATION AND CHARACTERIZATION OF THE  
; FILE REFERENCE: CSA OPERON  
; CURRENT APPLICATION NUMBER: US/09/839,894  
; CURRENT FILING DATE: 2001-04-20  
; PRIOR APPLICATION NUMBER: 60/198,626  
; PRIOR FILING DATE: 2000-04-20  
; NUMBER OF SEQ ID NOS: 40  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 38  
; LENGTH: 142  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: ETEC Protein Homology Sequence  
US-09-839-894-38

Query Match 67.6%; Score 46; DB 10; Length 142;  
Best Local Similarity 72.7%; Pred. No. 4.1;

Matches 8; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 2 TAGAPTAGNY 12

Db 113 TGTAPSNKTY 123

## RESULT 12

US-10-369-493-20514  
; Sequence 20514, Application US/10369493  
; Publication No. US20030233675A1  
; GENERAL INFORMATION:  
; APPLICANT: Cao, Yongwei  
; APPLICANT: Hinkle, Gregory J.  
; APPLICANT: Slater, Steven C.  
; APPLICANT: Goldman, Barry S.  
; APPLICANT: Chen, Xiandeng  
; TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION OF  
; FILE REFERENCE: 38-10(52052)B  
; CURRENT APPLICATION NUMBER: US/10/369,493  
; CURRENT FILING DATE: 2003-02-28  
; PRIOR APPLICATION NUMBER: US 60/360,039  
; PRIOR FILING DATE: 2002-02-21  
; NUMBER OF SEQ ID NOS: 47374  
; SEQ ID NO 20514  
; LENGTH: 980  
; TYPE: PRT  
; ORGANISM: Rhodospseudomonas palustris  
US-10-369-493-20514

Query Match 61.8%; Score 42; DB 12; Length 980;  
Best Local Similarity 70.0%; Pred. No. 1.5e+02;

Matches 7; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 3 AGTAPTAGNY 12

Db 864 AGTAPASGNF 873

## RESULT 13

US-10-224-125-20

; Sequence 20, Application US/10224125  
; Publication No. US20030161889A1  
; GENERAL INFORMATION:  
; APPLICANT: REID, ROBERT H.  
; APPLICANT: BOEDEKER, EDGAR C.  
; APPLICANT: VAN HAMONT, JOHN  
; APPLICANT: SETTERSTROM, JEAN A.  
; APPLICANT: MCQUEEN, CHARLES  
; APPLICANT: CASSELS, FREDERICK  
; TITLE OF INVENTION: VACCINES AGAINST DISEASES CAUSED BY ENTEROPATHOGENIC  
; TITLE OF INVENTION: ORGANISMS USING ANTIGENS ENCAPSULATED WITHIN  
; FILE REFERENCE: Army 108  
; CURRENT APPLICATION NUMBER: US/10/224,125  
; CURRENT FILING DATE: 2002-08-20  
; PRIOR APPLICATION NUMBER: 08/789,734  
; PRIOR FILING DATE: 1997-01-27  
; PRIOR APPLICATION NUMBER: 08/352,944  
; PRIOR FILING DATE: 1994-12-09  
; PRIOR APPLICATION NUMBER: 08/034,949  
; PRIOR FILING DATE: 1993-03-22  
; PRIOR APPLICATION NUMBER: 07/867,301  
; PRIOR FILING DATE: 1992-04-10  
; PRIOR APPLICATION NUMBER: 07/805,721  
; PRIOR FILING DATE: 1991-11-21  
; PRIOR APPLICATION NUMBER: 07/690,485  
; PRIOR FILING DATE: 1991-04-24  
; PRIOR APPLICATION NUMBER: 07/521,945  
; PRIOR FILING DATE: 1990-05-11  
; PRIOR APPLICATION NUMBER: 07/493,597  
; PRIOR FILING DATE: 1990-03-15  
; PRIOR APPLICATION NUMBER: 06/590,308  
; PRIOR FILING DATE: 1984-03-16  
; NUMBER OF SEQ ID NOS: 40  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 20  
; LENGTH: 8  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic  
; OTHER INFORMATION: peptide  
US-10-224-125-20

Query Match 60.3%; Score 41; DB 12; Length 8;  
Best Local Similarity 100.0%; Pred. No. 7.1e+05;  
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KTATAPT 8

Db 1 KTATAPT 8

## RESULT 14

US-10-001-245-213  
; Sequence 213, Application US/10001245  
; Publication No. US20030175312A1  
; GENERAL INFORMATION:  
; APPLICANT: HOLM, Jens  
; APPLICANT: IPSEN, Henrik  
; APPLICANT: LARSEN, Jorgen N.  
; APPLICANT: SPANGFORT, Michael D.  
; TITLE OF INVENTION: No. US20030175312A1 mutant allergens  
; FILE REFERENCE: 4305/1H942-US2  
; CURRENT APPLICATION NUMBER: US/10/001,245  
; CURRENT FILING DATE: 2001-11-15  
; PRIOR APPLICATION NUMBER: US 60/298,170  
; PRIOR FILING DATE: 2001-06-14  
; PRIOR APPLICATION NUMBER: US 60/249,361  
; PRIOR FILING DATE: 2000-11-16  
; NUMBER OF SEQ ID NOS: 217  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 213

LENGTH: 179  
TYPE: PRT  
ORGANISM: Hordeum vulgare  
US-10-001-245-213

Query Match 60.3%; Score 41; DB 12; Length 179;  
Best Local Similarity 80.0%; Pred. No. 36;  
Matches 8; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
Qy 3 AGTAPTAGNY 12  
Db 168 AGAATAGNY 177

## RESULT 15

US-10-001-245-212  
Sequence 212, Application US/10001245  
Publication No. US20030175312A1  
GENERAL INFORMATION:  
APPLICANT: HOLM, Jens  
APPLICANT: IPSEN, Henrik  
APPLICANT: LARSEN, Jorgen N.  
APPLICANT: SPANGFORT, Michael D.  
TITLE OF INVENTION: No. US20030175312A1 mutant allergens  
FILE REFERENCE: 4305/1H942-US2  
CURRENT APPLICATION NUMBER: US/10/001,245  
CURRENT FILING DATE: 2001-11-15  
PRIOR APPLICATION NUMBER: US 60/298,170  
PRIOR FILING DATE: 2001-06-14  
PRIOR APPLICATION NUMBER: US 60/249,361  
PRIOR FILING DATE: 2000-11-16  
NUMBER OF SEQ ID NOS: 217  
SOFTWARE: PatentIn version 3.1  
SEQ ID NO 212  
LENGTH: 313  
TYPE: PRT  
ORGANISM: Hordeum vulgare  
US-10-001-245-212

Query Match 60.3%; Score 41; DB 12; Length 313;  
Best Local Similarity 80.0%; Pred. No. 64;  
Matches 8; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
Qy 3 AGTAPTAGNY 12  
Db 302 AGAATAGNY 311

Search completed: February 6, 2004, 11:45:13  
Job time : 35 secs

GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: February 6, 2004, 11:37:30 / Search time 21 Seconds  
(without alignments)  
59.533 Million cell updates/sec

Title: US-09-618-577-28  
Perfect score: 68  
Sequence: 1 KTACTAPTAGNYS 13

Scoring table: BLOSUM62  
Gapop 10.0, Gapext 0.5

Searched: 283308 seqs, 96168682 residues  
Total number of hits satisfying chosen parameters: 283308

Minimum DB seq length: 0  
Maximum DB seq length: 200000000  
Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : PIR\_76: \*  
1: p1r1: \*  
2: p1r2: \*  
3: p1r3: \*  
4: p1r4: \*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	68	100.0	170	1 YOEBC1	CPAI fimbrial prot
2	68	100.0	170	2 B56617	colonization facto
3	46	67.6	359	2 S44738	C02C2.5 protein -
4	44	64.7	384	1 W2ML41	E2 protein - human
5	42	61.8	358	2 D83919	branched-chain ami
6	41	60.3	218	2 S29712	segmentation prote
7	41	60.3	313	2 JC5475	pollen allergen 9
8	41	60.3	560	2 S41808	glucose-6-phosphat
9	40	58.8	346	2 T51728	hypothetical prote
10	40	58.8	792	2 T20345	hypothetical prote
11	39	57.4	1791	2 T02345	hypothetical prote
12	39	57.4	212	2 B69522	hypothetical prote
13	39	57.4	256	2 T03371	glycine-rich prote
14	39	57.4	306	2 D70924	probable cdkA prot
15	39	57.4	333	2 A39098	allergen Poa p IX
16	39	57.4	333	2 A39098	hypothetical prote
17	38	55.9	124	1 H86350	trans-regulatory s
18	38	55.9	161	2 G72711	hypothetical prote
19	38	55.9	321	1 R5UBP0	acidic ribosomal p
20	38	55.9	343	2 R82755	transcription regu
21	38	55.9	363	2 S57763	branched-chain ami
22	38	55.9	430	2 JC4720	toxin co-regulated
23	38	55.9	723	2 T14765	hypothetical glyci
24	38	55.9	1079	2 B70807	hypothetical glyci
25	37	54.4	153	2 C72420	hypothetical prote
26	37	54.4	180	2 B83064	hypothetical prote
27	37	54.4	197	2 F75468	probable DNA polym
28	37	54.4	231	1 D64170	hypothetical prote
29	37	54.4	262	2 C71109	hypothetical prote

30	37	54.4	344	2 C70580	hypothetical prote
31	37	54.4	793	2 H82594	feric enterobacti
32	37	54.4	1145	2 T18235	transcription acti
33	37	54.4	1557	2 T28811	hypothetical prote
34	37	54.4	1787	2 AG1360	probable tape-meas
35	37	54.4	1788	2 AH1447	probable tape-meas
36	37	54.4	1815	2 B95942	conserved hypotet
37	36	52.9	53	2 S18013	protein-tyrosine k
38	36	52.9	163	2 JQ0139	hypothetical 17.8k
39	36	52.9	257	2 G36810	hypothetical prote
40	36	52.9	261	2 D75335	hypothetical prote
41	36	52.9	310	2 B73476	conserved hypotet
42	36	52.9	352	2 S16547	neutral proteinase
43	36	52.9	356	2 H69750	branched-chain ami
44	36	52.9	390	2 G82844	cysteine synthase
45	36	52.9	415	2 A35560	lysosomal membrane

## ALIGNMENTS

RESULT 1  
YOEBC1  
CPAI fimbrial protein precursor - Escherichia coli  
N/Alternate names: CPAI pili; colonization factor antigen I (CPAI)  
C/Species: Escherichia coli  
C/Date: 14-Nov-1983 #sequence revision 30-Jun-1991 #text\_change 15-Nov-1996  
C/Accession: A30589; A03495; A43831  
R/Karjalainen, T.K.; Evans, D.G.; So, M.; Lee, C.H.  
Infect. Immun. 57, 1126-1130, 1989  
A/Title: Molecular cloning and nucleotide sequence of the colonization factor antigen I  
A/Reference number: A30589; MUID:89173309; PMID:2564374  
A/Accession: A30589  
A/Molecule type: DNA  
A/Residues: 1-170 <KAR>  
R/Klemp, P.  
Eur. J. Biochem. 124, 339-348, 1982  
A/Title: Primary structure of the CPAI fimbrial protein from human enterotoxigenic Esche  
A/Reference number: A03495; MUID:82235736; PMID:6124420  
A/Accession: A03495  
A/Molecule type: DNA  
A/Residues: 24-75, 'N', 77-96, 'A', 98-170 <KLE>  
R/Cassels, F.J.; Deal, C.D.; Reid, R.H.; Jarboe, D.L.; Naus, J.L.; Carter, J.M.; Boedek  
Infect. Immun. 60, 2174-2181, 1992  
A/Title: Analysis of Escherichia coli colonization factor antigen I linear B-cell epitope  
A/Reference number: A43831; MUID:92267624; PMID:1375193  
A/Accession: A43831  
A/Molecule type: protein  
A/Residues: 24-170 <CAS>  
A/Experimental source: strain H10407  
A/Note: Sequence extracted from NCBI backbone (NCBIP:104220)  
C/Comment: The CPAI fimbriae are rather rigid, thread-like filaments of 0.5-1 micrometer,  
tical protein subunits.  
C/Superfamily: CPAI fimbrial protein  
C/Keywords: fimbria  
F:1-23/Domain: signal sequence #status predicted <SIG>  
F:24-170/Product: CPAI fimbrial protein #status experimental <MAT>  
Query Match 100.0%; Score 68; DB 1; Length 170;  
Best Local Similarity 100.0%; Pred. No. 0.00015;  
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
OY 1 KTACTAPTAGNYS 13  
DB 147 KTACTAPTAGNYS 159  
RESULT 2  
B56617  
colonization factor antigen I precursor - Escherichia coli plasmid NTP113  
C/Species: Escherichia coli  
C/Date: 05-Jan-1996 #sequence\_revision 05-Jan-1996 #text\_change 03-May-1996

C:Accession: B56617  
 R:Jordi, B.T.; Willehaw, G.A.; van der Zeijst, B.A.; Gaaststra, W.  
 DNA Seq. 2, 257-263, 1992  
 A>Title: The complete nucleotide sequence of region 1 of the CFA/I fimbrial operon of hu  
 A:Reference number: A56617; MUID:92329981; PMID:1352712  
 A:Accession: B56617  
 A:Status: preliminary  
 A:Molecule type: DNA  
 A:Residues: 1-170 <OR>  
 A:Experimental source: enterotoxigenic strain, CFA/I-ST plasmid NTP113  
 A>Note: sequence inconsistent with nucleotide translation  
 A>Note: sequence extracted from NCBI backbone (NCBIN:108960, NCBI:108970)  
 C:Genetics:  
 A:Gene: cfab  
 A:Genome: plasmid  
 C:Superfamily: CFAI fimbrial protein

Query Match 100.0%; Score 68; DB 2; Length 170;  
 Best Local Similarity 100.0%; Pred. No. 0.00015;  
 Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KTAGTAPTAGNYS 13  
 |||||  
 Db 147 KTAGTAPTAGNYS 159

RESULT 3  
 S44738  
 C02C2.5 protein - Caenorhabditis elegans  
 C:Species: Caenorhabditis elegans  
 C:Date: 08-Sep-1994 #sequence\_revision 10-Nov-1995 #text\_change 09-Sep-1997  
 C:Accession: S44738  
 R:Wilson, R.  
 submitted to the EMBL Data Library, September 1993  
 A:Description: Sequence of the C. elegans cosmid C02C2.  
 A:Reference number: S44738  
 A:Accession: S44738  
 A:Status: preliminary  
 A:Molecule type: DNA  
 A:Residues: 1-359 <NUL>  
 A:Cross-references: EMBL:L23649; NID:g388566; PID:g388568  
 C:Genetics:  
 A:introns: 69/3; 101/3; 127/3; 178/1; 219/2; 252/3; 313/1

Query Match 67.6%; Score 46; DB 2; Length 359;  
 Best Local Similarity 72.7%; Pred. No. 2.2;  
 Matches 8; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 KTAGTAPTAGN 11  
 |||||  
 Db 175 KTAGTSPSVGN 185

RESULT 4  
 W2ML41  
 E2 protein - human papillomavirus type 41  
 C:Species: human papillomavirus type 41  
 A>Note: host Homo sapiens (man)  
 C:Date: 30-Jun-1993 #sequence\_revision 30-Jun-1993 #text\_change 16-Feb-1997  
 C:Accession: D43550  
 R:Hirt, L.; Hirsch-Benam, A.; De Villiers, E.M.  
 Virus Res. 18, 179-190, 1990  
 A>Title: Nucleotide sequence of human papillomavirus (HPV) type 41: an unusual HPV type  
 A:Reference number: A43550  
 A:Accession: D43550  
 A:Status: translation not shown  
 A:Molecule type: DNA  
 A:Residues: 1-384 <HIR>  
 A:Cross-references: EMBL:X56147  
 C:Superfamily: papillomavirus E2 protein  
 A:Keywords: DNA binding; early protein; transcription regulation  
 Query Match 64.7%; Score 44; DB 1; Length 384;

Best Local Similarity 66.7%; Pred. No. 5.3;  
 Matches 8; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 1 KTAGTAPTAGNYS 12  
 |||||  
 Db 291 KTAGVAPAEGRY 302

RESULT 5  
 D83919  
 branched-chain amino acid aminotransferase bcat [imported] - Bacillus halodurans (strain  
 C:Species: Bacillus halodurans  
 C:Date: 01-Dec-2000 #sequence\_revision 01-Dec-2000 #text\_change 15-Jun-2001  
 R:Takami, H.; Nakasone, K.; Takaki, Y.; Maeno, G.; Sasaki, R.; Masui, N.; Fujii, F.; Hiran  
 Nucleic Acids Res. 28, 4317-4331, 2000  
 A>Title: Complete genome sequence of the alkaliphilic bacterium Bacillus halodurans and  
 A:Reference number: A83650; MUID:20512582; PMID:11058132  
 A:Accession: D83919  
 A:Status: preliminary  
 A:Molecule type: DNA  
 A:Residues: 1-358 <STO>  
 A:Cross-references: GB:AP001514; GB:BA000004; NID:q10174613; PIDN:BA05875.1; GSPDB:GN001  
 A:Experimental source: strain C-125  
 C:Genetics:  
 A:Gene: bcat  
 C:Superfamily: branched-chain-amino-acid transaminase BAT1

Query Match 61.8%; Score 42; DB 2; Length 358;  
 Best Local Similarity 80.0%; Pred. No. 11;  
 Matches 8; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 4 GTAPTAGNYS 13  
 |||||  
 Db 194 GTAPTGNYS 203

RESULT 6  
 S29712  
 segmentation protein hairy - red flour beetle  
 C:Species: Tribolium castaneum (red flour beetle)  
 C:Date: 19-Mar-1997 #sequence\_revision 01-Aug-1997 #text\_change 17-Mar-1999  
 C:Accession: S29712  
 R:Sommer, R.J.; Tautz, D.  
 Nature 361, 448-450, 1993  
 A>Title: Involvement of an orthologue of the Drosophila pair-rule gene hairy in segment  
 A:Reference number: S29712; MUID:93156810; PMID:8429884  
 A:Accession: S29712  
 A:Status: preliminary  
 A:Molecule type: DNA  
 A:Residues: 1-218 <SOM>

Query Match 60.3%; Score 41; DB 2; Length 218;  
 Best Local Similarity 61.5%; Pred. No. 9.9;  
 Matches 8; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 1 KTAGTAPTAGNYS 13  
 |||||  
 Db 169 KTASTASASNYS 181

RESULT 7  
 JCS475  
 pollen allergen 9 precursor - barley  
 N:Alternate names: Hor v 9  
 C:Species: Hordeum vulgare (barley)  
 C:Date: 07-Jul-1997 #sequence\_revision 29-Aug-1997 #text\_change 20-Aug-1999  
 C:Accession: JCS475  
 R:Aswood, J.D.; Hill, R.D.  
 Gene 182, 53-62, 1996  
 A>Title: Cloning and expression pattern of Hor v 9, the group 9 pollen isoallergen from  
 A:Reference number: JCS475; MUID:97136690; PMID:8982067  
 A:Accession: JCS475

A:Molecule type: mRNA  
A:Residues: 1-313 <AST>  
A:Cross-references: GB:U57845; NID:G1808986; PIDN:AB41585.1; PID:G1808987  
C:Comment: This protein belongs to group 9 pollen allergen.  
C:Superfamily: grass pollen allergen IX  
F1-27/Domain: signal sequence #status predicted <SIG>  
F1-28-313/Product: pollen allergen #status predicted <MAT>  
F1-290-309/Domain: transmembrane #status predicted <TM>

Query Match 60.3%; Score 41; DB 2; Length 313;  
Best Local Similarity 80.0%; Pred. No. 14;  
Matches 8; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 3 AGTAPTAGNY 12  
|||  
Db 302 AGAATAGNY 311

RESULT 8  
S41808  
glucose-6-phosphate isomerase (EC 5.3.1.9), cytosolic - Arabidopsis thaliana  
N:Alternate names: phosphoglucose isomerase  
C:Species: Arabidopsis thaliana (mouse-ear cress)  
C>Date: 20-May-1994 #sequence\_revision 10-Nov-1995 #text\_change 16-Jul-1999  
C:Accession: S41808  
R:Thomas, B.R.; Ford, V.S.; Pichersky, E.; Gottlieb, L.D.  
Genetics 135, 895-905, 1993  
A>Title: Molecular characterization of duplicate cytosolic phosphoglucose isomerase gene  
A:Reference number: S41806; MUID:94123980; PMID:8293986  
A:Accession: S41808  
A:Molecule type: DNA  
A:Residues: 1-560 <THO>  
A:Cross-references: EMBL:X69195; NID:G415922; PIDN:CAA48940.1; PID:G415923  
C:Genetics:  
A:Gene: pgic  
A:Introns: 18/3; 44/2; 71/3; 87/3; 139/3; 172/1; 186/2; 209/1; 237/2; 253/3; 278/1; 298/  
C:Superfamily: glucose-6-phosphate isomerase  
C:Keywords: cytosol; gluconeogenesis; glycolysis; intramolecular oxidoreductase; isomere

Query Match 60.3%; Score 41; DB 2; Length 560;  
Best Local Similarity 61.5%; Pred. No. 26;  
Matches 8; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

OY 1 KTAGTAPTAGNY 13  
:|||||  
Db 531 RTGTAPEGFNYS 543

RESULT 9  
T51728  
hypothetical protein [imported] - Arabidopsis thaliana  
C:Species: Arabidopsis thaliana (mouse-ear cress)  
C>Date: 18-Aug-2000 #sequence\_revision 18-Aug-2000 #text\_change 18-Aug-2000  
C:Accession: T51728  
R:Olney, M.A.; Briggs, W.R.  
submitted to the EMBL Data Library, August 1998  
A:Description: Arabidopsis thaliana mRNA of unknown function.  
A:Reference number: Z25441  
A:Accession: T51728  
A:Status: preliminary; translated from GB/EMBL/DBJ  
A:Molecule type: mRNA  
A:Residues: 1-346 <OLN>  
A:Cross-references: EMBL:AF087435; PIDN:AAD1574.1  
A:Experimental source: cultivar Columbia

Query Match 58.8%; Score 40; DB 2; Length 346;  
Best Local Similarity 72.7%; Pred. No. 24;  
Matches 8; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

OY 1 KTAGTAPTAGN 11  
|||||  
Db 304 KTAGPAPTYGH 314

RESULT 10  
T26050  
hypothetical protein W01C9.3 - Caenorhabditis elegans  
C:Species: Caenorhabditis elegans  
C>Date: 15-Oct-1999 #sequence\_revision 15-Oct-1999 #text\_change 15-Oct-1999  
C:Accession: T26050  
R:Sims, M.  
submitted to the EMBL Data Library, June 1995  
A:Reference number: Z20143  
A:Accession: T26050  
A:Status: preliminary; translated from GB/EMBL/DBJ  
A:Molecule type: DNA  
A:Residues: 1-792 <WIL>  
A:Cross-references: EMBL:Z49969; PIDN:CAA90267.1; GSPDB:GN00020; CESP:W01C9.3  
A:Experimental source: clone W01C9  
C:Genetics:  
A:Gene: CESP:W01C9.3  
A:Map position: 2  
A:Introns: 15/1; 40/1; 66/3; 101/3; 182/2; 270/3; 338/3; 366/1; 597/3; 613/2; 646/2; 684/  
Query Match 58.8%; Score 40; DB 2; Length 792;  
Best Local Similarity 58.3%; Pred. No. 56;  
Matches 7; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

OY 1 KTAGTAPTAGNY 12  
:|||||  
Db 251 QTAGSPPIKXNY 262

RESULT 11  
T02345  
hypothetical protein KIAA0324 - human (fragment)  
C:Species: Homo sapiens (man)  
C>Date: 05-Mar-1999 #sequence\_revision 05-Mar-1999 #text\_change 05-Nov-1999  
C:Accession: T02345  
R:Rickey, D.O.; Bruce, D.; Mundt, M.; Doggett, N.; Munk, C.; Saunders, E.; Robinson, D.;  
re, J.; White, S.; Ueng, S.; Tatum, O.; Campbell, C.; Fawcett, J.; Deaven, L.  
submitted to the EMBL Data Library, March 1998  
A:Description: Sequencing of human chromosome 16p13.3.  
A:Reference number: Z14664  
A:Accession: T02345  
A:Status: preliminary; translated from GB/EMBL/DBJ  
A:Molecule type: DNA  
A:Residues: 1-1791 <RIC>  
A:Cross-references: EMBL:AC004493; NID:G2996648; PIDN:AAC08453.1; PID:G2996650  
C:Genetics:  
A:Map position: 16  
A:Introns: 1610/2; 1706/2  
A>Note: KIAA0324

Query Match 58.8%; Score 40; DB 2; Length 1791;  
Best Local Similarity 70.0%; Pred. No. 1.3e+02;  
Matches 7; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

OY 3 AGTAPTAGNY 12  
:|||||  
Db 1346 GTTPTTANY 1355

RESULT 12  
BE9522  
hypothetical protein AF2181 - Archaeoglobus fulgidus  
C:Species: Archaeoglobus fulgidus  
C>Date: 05-Dec-1997 #sequence\_revision 05-Dec-1997 #text\_change 22-Oct-1999  
C:Accession: BE9522  
R:Klenk, H.P.; Clayton, R.A.; Tomb, J.F.; White, O.; Nelson, K.E.; Ketchum, K.A.; Dodson,  
.; Fleischmann, R.D.; Quackenbush, J.; Lee, N.H.; Sutton, G.G.; Gill, S.; Kirkness, E.F.;  
Glodek, A.; Zhou, L.; Overbeek, R.; Gocayne, J.D.; Weidman, J.F.; McDonald, L.  
Nature 390, 364-370, 1997  
A:Authors: Usterback, T.; Cotton, M.D.; Spriggs, T.; Artlich, P.; Kaine, B.P.; Sykes, S.N.  
Smith, H.O.; Woese, C.R.; Venter, J.C.  
A>Title: The complete genome sequence of the hyperthermophilic, sulfate-reducing archaeo

A:Reference number: A69250; MUID:98049343; PMID:9389475  
 A:Accession: E69522  
 A:Status: preliminary; nucleic acid sequence not shown; translation not shown  
 A:Molecule type: DNA  
 A:Residues: 1-212 <KLE>  
 A:Cross-references: GB:AE000954; GB:AE000782; NID:g2689277; PIDN:AA89076.1; PID:g264834

Query Match 57.4%; Score 39; DB 2; Length 212;  
 Best Local Similarity 72.7%; Pred. No. 22;  
 Matches 8; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 3 AGTAPTAGNYS 13  
 |||  
 DB 132 AGAALAGNYS 142

#### RESULT 13

T03371  
 glycine-rich protein grp3 - maize

C:Species: Zea mays (maize)  
 C:Date: 24-Mar-1999 #sequence\_revision 24-Mar-1999 #text\_change 21-Jul-2000  
 C:Accession: T03371

R:Godeffroy, M.L.; Muller, D.; Felix, G.

Plant Mol. Biol. 36: 799-802, 1998

A:Title: Root-specific expression of a Zea mays gene encoding a novel glycine-rich protein

A:Reference number: Z14904; MUID:98187261; PMID:9526513

A:Accession: T03371

A:Status: preliminary; translated from GB/EMBL/DBJ

A:Residues: 1-256 <GOD>

A:Cross-references: EMBL:Y07781; NID:g1532070; PIDN:CA69104.1; PID:g1532071

A:Experimental source: strain DK105; root

C:Genetics:

A:Gene: grp3

C:Superfamily: glycine-rich cell wall structural protein 1

Query Match 57.4%; Score 39; DB 2; Length 256;  
 Best Local Similarity 50.0%; Pred. No. 26;  
 Matches 6; Conservative 4; Mismatches 2; Indels 0; Gaps 0;

QY 2 TAGTAPTAGNYS 13  
 |||  
 DB 114 TAGSPSSGNVA 125

#### RESULT 14

D70924

probable cda protein - Mycobacterium tuberculosis (strain H37RV)

C:Species: Mycobacterium tuberculosis

C:Date: 17-Jul-1998 #sequence\_revision 17-Jul-1998 #text\_change 20-Jun-2000

C:Accession: D70924

R:Cole, S.T.; Broesch, R.; Parthill, J.; Garnier, T.; Churcher, C.; Harris, D.; Gordon, S.

Connor, R.; Davies, R.; Devlin, K.; Fellwell, T.; Gentles, S.; Hamlin, N.; Holroyd, S.

Rajandream, M.A.; Rogers, J.; Rutter, S.; Seeger, K.; Skelton, S.; Squares, S.

Nature 393, 537-544, 1998

A:Authors: Squares, R.; Sulston, J.E.; Taylor, K.; Whitehead, S.; Barrell, B.G.

A:Title: Deciphering the biology of Mycobacterium tuberculosis from the complete genome

A:Reference number: A70500; MUID:98295987; PMID:9634230

A:Accession: D70924

A:Status: preliminary; nucleic acid sequence not shown; translation not shown

A:Molecule type: DNA

A:Residues: 1-306 <COL>

A:Cross-references: GB:Z74024; GB:AL123456; NID:g1250700; PIDN:CA98357.1; PID:g1403401

A:Experimental source: strain H37RV

C:Genetics:

A:Gene: cda

C:Superfamily: phosphatidate cytidyltransferase

Query Match 57.4%; Score 39; DB 2; Length 306;  
 Best Local Similarity 63.6%; Pred. No. 31;  
 Matches 7; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 2 TAGTAPTAGNY 12

DB 135 TTGAPSPGNV 145  
 |||

#### RESULT 15

A39098

allergen Poa p IX (clone 41) - Kentucky bluegrass

C:Species: Poa pratensis (Kentucky bluegrass)

C:Date: 27-Nov-1991 #sequence\_revision 03-Apr-1992 #text\_change 20-Aug-1999

C:Accession: A39098

R:Silvanovich, A.; Astwood, J.; Zhang, L.; Olsen, E.; Kissel, F.; Sehon, A.; Mohapatra, S.

J. Biol. Chem. 266, 1204-1210, 1991

A:Title: Nucleotide sequence analysis of three cDNAs coding for Poa p IX isoallergens of

A:Reference number: A39098; MUID:91093232; PMID:1702432

A:Accession: A39098

A:Status: preliminary

A:Molecule type: mRNA

A:Residues: 1-333 <SLI>

A:Cross-references: GB:M38343; NID:g169628; PIDN:AA63456.1; PID:g169629

A:Note: the authors translated the codon GCG for residue 296 as Ser

C:Superfamily: grass pollen allergen IX

C:Keywords: pollen

Query Match 57.4%; Score 39; DB 2; Length 333;  
 Best Local Similarity 58.3%; Pred. No. 34;  
 Matches 7; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 1 KTAGTAPTAGNY 12  
 |||  
 DB 320 KTGAATPTAGCY 331

Search completed: February 6, 2004, 11:39:25  
 Job time : 23 secs

GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: February 6, 2004, 11:37:30; Search time 11 Seconds  
(without alignments)  
55.577 Million cell updates/sec

Title: US-09-618-577-28

Percent score: 68

Sequence: 1 KTACTGAPTAGNYS 13

Scoring table: BLOSUM62  
Gapop 10.0, Gapext 0.5

Searched: 127863 seqs, 47026705 residues

Total number of hits satisfying chosen parameters: 127863

Minimum DB seq length: 0  
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%  
Maximum Match 100%

Listing first 45 summaries

Database: SwissProt\_41.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	68	100.0	170	1	FMCI_ECOLI
2	46	67.6	359	1	YKH5_CABEL
3	44	64.7	387	1	V22_HPV41
4	41	60.3	560	1	G6P1_ARATH
5	39	57.4	212	1	YL81_ARCFU
6	39	57.4	306	1	CDS4_MYCTU
7	39	57.4	330	1	A85B_MYCSC
8	39	57.4	333	1	MP92_POAPR
9	38	55.9	124	1	REV_STVCZ
10	38	55.9	321	1	PLA6_CHERU
11	38	55.9	362	1	ILVE_BACSV
12	38	55.9	364	1	VSGP_EBOC
13	38	55.9	364	1	VSGP_EBOC
14	38	55.9	364	1	VSGP_EBOC
15	38	55.9	430	1	TCPB_VIBCH
16	38	55.9	676	1	VGP_EBOEC
17	38	55.9	676	1	VGP_EBOG4
18	38	55.9	676	1	VGP_EBOZ5
19	38	55.9	676	1	VGP_EBOZM
20	37	54.4	231	1	YOHK_HAEIN
21	37	54.4	1535	1	LM11_CABEL
22	36	52.9	257	1	VG45_HSVGA
23	36	52.9	352	1	NP11_ASFOR
24	36	52.9	356	1	YBGE_BACSV
25	36	52.9	415	1	LMF2_MOUSE
26	36	52.9	480	1	TMG2_HUMAN
27	36	52.9	521	1	IMH3_CANAL
28	36	52.9	666	1	FLID_VIBCH
29	36	52.9	717	1	ARA_BROME
30	36	52.9	769	1	ZBR2_CHICK
31	36	52.9	929	1	SPB3_YEAST
32	36	52.9	936	1	CAP1_RHOPA
33	36	52.9	1620	1	ALK_HUMAN

34	36	52.9	5703	1	MUSEB_HUMAN	Q9hce4 homo sapien
35	35.5	52.2	513	1	COX1_HUMAN	P00395 homo sapien
36	35.5	52.2	514	1	COX1_PONDA	P26992 pongo pygma
37	35	51.5	363	1	ALFB_CHICK	P07341 gallus galli
38	35	51.5	372	1	VSGP_EBOC	O89455 ebola virus
39	35	51.5	401	1	P39_BRUBA	O06875 brucella ab
40	35	51.5	482	1	T2EA_YEAST	P36100 saccharomyc
41	35	51.5	511	1	AMYC_HUMAN	P19961 homo sapien
42	35	51.5	511	1	AMYF_HUMAN	P04746 homo sapien
43	35	51.5	511	1	AMYS_HUMAN	P04745 homo sapien
44	35	51.5	540	1	PLIF_BRUBA	O52069 brucella ab
45	35	51.5	547	1	MUTL_DEIRA	Q9rtt0 deinococcus

#### ALIGNMENTS

RESULT 1  
FMCI\_ECOLI STANDARD; PRT; 170 AA.  
ID FMCI\_ECOLI  
AC P02971;  
DT 21-JUL-1986 (Rel. 01, Created)  
DT 01-FEB-1991 (Rel. 17, Last sequence update)  
DT 15-JUL-1999 (Rel. 38, Last annotation update)  
DE CFA/I fimbrial subunit B precursor (Colonization factor antigen I subunit B) (CFA/I pilin) (CFA/I antigen).  
GN CPAB.  
OS Escherichia coli.  
OC Plasmid NTP513.  
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;  
OC Enterobacteriaceae; Escherichia.  
OX NCBI\_TaxID=562;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=89173309; PubMed=2564374;  
RA Karjalainen T.K., Evans D.G., So M., Lee C.-H.;  
RT "Molecular cloning and nucleotide sequence of the colonization factor antigen I gene of Escherichia coli.";  
RL Infect. Immun. 57:1126-1130(1989).  
RN [2]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=89330163; PubMed=2569152;  
RA Hamers A.M., Pel H.J., Wilshaw G.A., Kusters J.G.,  
RA van der Zeijst B.A.M., Gaastra W.;  
RT "The nucleotide sequence of the first two genes of the CFA/I fimbrial operon of human enterotoxigenic Escherichia coli.";  
RL Microb. Pathog. 6:297-309(1989).  
RN [3]  
RP SEQUENCE OF 24-170 FROM N.A.  
RX STRAIN=O78:H11 / H10407;  
RA Hall R.H., Maneval D.R. Jr., Collins J.H., Theibert J.L.,  
RA Levine M.M.;  
RT "Purification and analysis of colonization factor antigen I, coli enterotoxigenic Escherichia coli.";  
RL J. Bacteriol. 171:6372-6374(1989).  
RN [4]  
RP SEQUENCE OF 24-42.  
RX STRAIN=O78:H11 / H10407;  
RA MEDLINE=90036735; PubMed=2572583;  
RA Hall R.H., Maneval D.R. Jr., Collins J.H., Theibert J.L.,  
RA Levine M.M.;  
RT "Purification and analysis of colonization factor antigen I, coli enterotoxigenic Escherichia coli.";  
RL J. Bacteriol. 171:6372-6374(1989).  
RN [5]  
RP FUNCTION: FIMBRIAE (ALSO CALLED PILI), POLAR FILAMENTS RADIATING FROM THE SURFACE OF THE BACTERIUM TO A LENGTH OF 0.5-1.5 MICROMETERS AND NUMBERING 100-300 PER CELL, ENABLE BACTERIA TO COLONIZE THE EPITHELIUM OF SPECIFIC HOST ORGANS.  
CC - SUBUNIT: CFA/I FIMBRIAE ARE RATHER RIGID, THREAD-LIKE FILAMENTS OF 0.5-1 MICROMETER, WITH AN APPARENT AXIAL HOLE, AND A DIAMETER OF 7 NANOMETERS. A SINGLE CFA/I FIMBRIA CONSISTS OF ABOUT 100 IDENTICAL PROTEIN SUBUNITS.

```

CC -1- INDUCTION: CFA/I FIMBRIAE ARE ONLY EXPRESSED IN THE PRESENCE OF
CC THE POSITIVE REGULATOR CFAD.
CC -1- SIMILARITY: TO THE CSI FIMBRIAL SUBUNIT A (CSOA).
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
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CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
CC -----
CC EMBL: M55661; AAC4145.1; -.
CC PIR: A30589; YOECC1.
CC Pfam: PF04449; Fimbrial_CSI; 1.
CC Fimbrin; Antigen; Plasmid; Signal.
CC SIGNAL
CC FT CHAIN 1 23
CC FT CONFLICT 24 170 CFA/I FIMBRIAL SUBUNIT B.
CC FT CONFLICT 37 37 V -> A (IN REF. 2).
CC FT CONFLICT 76 76 D -> N (IN REF. 3).
CC FT CONFLICT 97 97 S -> A (IN REF. 3).
CC SEQUENCE 170 AA; 17461 MW; 92434707F33CDAB CRC64;
CC
CC Query Match 100.0%; Score 68; DB 1; Length 170;
CC Best Local Similarity 100.0%; Pred. No. 7.7e-05;
CC Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
CC
CC QY 1 KTAGTAPTAGNYS 13
CC DB 147 KTAGTAPTAGNYS 159
CC
CC RESULT 2
CC YKHS CAEEL
CC ID YKHS CAEEL STANDARD; PRT; 359 AA.
CC AC P34273;
CC DT 01-FEB-1994 (Rel. 28, Created)
CC DT 01-FEB-1994 (Rel. 28, Last sequence update)
CC DT 28-FEB-2003 (Rel. 41, Last annotation update)
CC DE Hypothetical protein C02C2.5 in chromosome III.
CC GN C02C2.5
CC OS Caenorhabditis elegans.
CC OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
CC OC Rhabditidae; Peloderinae; Caenorhabditis.
CC OX NCBI_TaxId=6239;
CC RN [1]
CC RP SEQUENCE FROM N.A.
CC RC STRAIN=Bristol N2;
CC RX MEDLINE=94150718; PubMed=7906398;
CC RA Wilson R., Alnough R., Anderson K., Baynes C., Berks M.,
CC RA Bonfield J., Burton J., Connell M., Copsey T., Cooper J., Coulson A.,
CC RA Craxton M., Dear S., Du Z., Durbin R., Favell A., Fraser A.,
CC RA Fulton L., Garner A., Green P., Hawkins T., Hillier L., Jier M.,
CC RA Johnston L., Jones M., Kershaw J., Kirsten J., Laister N.,
CC RA Latreille P., Lightning J., Lloyd C., Mortimore B., O'Callaghan M.,
CC RA Parsons J., Percy C., Ritten L., Roopra A., Saunders D., Shownkeen R.,
CC RA Sims M., Smalton N., Smith A., Smith K., Sonhammer E., Staden R.,
CC RA Sulterson J., Thierry-Mieg J., Thomas K., Vaudin M., Vaughan K.,
CC RA Waterston R., Watson A., Weinstock L., Wilkinson-Sprat J.,
CC RA Wohldman P.;
CC RA "2.2 Mb of contiguous nucleotide sequence from chromosome III of C.
CC RT elegans.";
CC RL Nature 368:32-38(1994).
CC
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CC -----
CC EMBL: L23649; AAA27908.1; -.

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DR PIR: S44738; S44738.
DR WormPep; C02C2.5; CE00031.
DR InterPro; IPR000415; Nitroreductase.
DR Pfam; PF00881; Nitroreductase; 1.
DR KW Hypothetical protein.
DR SEQUENCE 359 AA; 41326 MW; BCC9450C72FFB780 CRC64;
DR
DR Query Match 67.6%; Score 46; DB 1; Length 359;
DR Best Local Similarity 72.7%; Pred. No. 1;
DR Matches 8; Conservative 2; Mismatches 1; Indels 0; Gaps 0;
DR
DR QY 1 KTAGTAPTAGN 11
DR DB 175 KTAGTAPSEVN 185
DR
DR RESULT 3
DR VE2_HPV41
DR ID VE2_HPV41 STANDARD; PRT; 387 AA.
DR AC P27552;
DR DT 01-AUG-1992 (Rel. 23, Created)
DR DT 01-AUG-1992 (Rel. 23, Last sequence update)
DR DT 15-JUN-1998 (Rel. 36, Last annotation update)
DR DE Regulatory protein E2.
DR GN E2.
DR OS Human papillomavirus type 41.
DR OC Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
DR OC Papillomavirus.
DR OX NCBI_TaxId=10589;
DR RN [1]
DR RP SEQUENCE FROM N.A.
DR RX MEDLINE=91253264; PubMed=1645904;
DR RA Hirt L., Hirsch-Benham A., de Villiers E.M.;
DR RT "Nucleotide sequence of human papillomavirus (HPV) type 41: an
DR RT unusual HPV type without a typical E2 binding site consensus
DR RT sequence.";
DR RL Virus Res. 18:119-190(1991).
DR
DR -1- FUNCTION: E2 REGULATES VIRAL TRANSCRIPTION AND DNA REPLICATION.
DR IT BINDS TO THE E2RE RESPONSE ELEMENT (5'-ACNNNNNGCT-3') PRESENT
DR IN MULTIPLE COPIES IN THE REGULATORY REGION. IT CAN EITHER
DR ACTIVATE OR REPRESS TRANSCRIPTION DEPENDING ON E2RE'S POSITION
DR WITH REGARDS TO PROXIMAL PROMOTER ELEMENTS. REPRESSION OCCURS
DR BY STERICALLY HANDERING THE ASSEMBLY OF THE TRANSCRIPTION
DR INITIATION COMPLEX. THE E1-E2 COMPLEX BINDS TO THE ORIGIN OF DNA
DR REPLICATION.
DR -1- SUBUNIT: Binds DNA as a dimer.
DR -1- SUBCELLULAR LOCATION: Nuclear.
DR
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DR or send an email to license@isb-sib.ch).
DR -----
DR EMBL: X56147; CAA39615.1; -.
DR PIR: D43550; W2WL41.
DR DR InterPro; IPR000427; E2_C.
DR DR InterPro; IPR001866; E2_N.
DR DR Pfam; PF00511; E2_C; 1.
DR DR Pfam; PF00508; E2_N; 1.
DR DR Pfam; PF00672; E2_C; 1.
DR DR Pfam; PF00678; E2_N; 1.
DR DR Early protein; Transcription regulation; Activator; DNA-binding;
DR KW Trans-acting factor; DNA replication; Repressor; Nuclear protein.
DR SEQUENCE 387 AA; 44230 MW; 8F9AA2C0395DBE848 CRC64;
DR
DR Query Match 64.7%; Score 44; DB 1; Length 387;
DR Best Local Similarity 66.7%; Pred. No. 2.5;
DR Matches 8; Conservative 1; Mismatches 3; Indels 0; Gaps 0;
DR
DR QY 1 KTAGTAPTAGN 12

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Db 294 KTGAAPAEGRHY 305

## RESULT 4

G6PI\_ARATH STANDARD, PRT; 560 AA.  
 ID G6PI\_ARATH STANDARD, PRT; 560 AA.  
 AC P34795; Q9FE90; Q9FXM6; Q9FXM7; Q9FXM8; Q9FXM9; Q9FXN0; Q9FXN1;  
 AC Q9FXN2; Q9FXN3; Q9FXN4; Q9FXN5;  
 DT 01-FEB-1994 (Rel. 28, Created)  
 DT 01-FEB-1994 (Rel. 28, Last annotation update)  
 DT 26-FEB-2003 (Rel. 41, Last annotation update)  
 DE Glucose-6-phosphate isomerase, cytosolic (EC 5.3.1.9) (GPI)  
 DE (Phosphoglucose isomerase) (PGI) (Phosphohexose isomerase) (PHI).  
 GN PGIC OR AT5G42740 OR MJB21.12.  
 OS Arabidopsis thaliana (Mouse-ear cress).  
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;  
 OC eustoids II; Brassicales; Brassicaceae; Arabidopsis.  
 OC NCB1\_TaxID=3702;  
 [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=cv. Columbia;  
 RX MEDLINE=94123980; PubMed=8293986;  
 RA Thomas B.R., Ford V.S., Pichersky E., Gottlieb L.D.;  
 RT "Molecular characterization of duplicate cytosolic phosphoglucose  
 RT isomerase genes in *Clarkia* and comparison to the single gene in  
 RT Arabidopsis";  
 RL Genetics 135:895-905 (1993).  
 [2]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=Many cultivars;  
 RA Kawabe A., Yamane K., Miyashita N.T.;  
 RT "DNA polymorphism at the cytosolic phosphoglucose isomerase (Pgic)  
 RT locus of the wild plant Arabidopsis thaliana";  
 RL Submitted (JUN-2000) to the EMBL/GenBank/DBJ databases.  
 [3]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=cv. Columbia;  
 RX MEDLINE=98162728; PubMed=9501997;  
 RA Nakamura Y., Sato S., Kaneko T., Kotani H., Asamizu E., Miyajima N.,  
 RA Tabata S.;  
 RT "Structural analysis of Arabidopsis thaliana chromosome 5. III.  
 RT Sequence features of the regions of 1,191,918 bp covered by seventeen  
 RT physically assigned P1 clones";  
 RL DNA Res. 4:401-414 (1997).  
 CC -1- CATALYTIC ACTIVITY: D-glucose 6-phosphate = D-fructose 6-  
 CC phosphate.  
 CC -1- PATHWAY: Involved in glycolysis and in gluconeogenesis.  
 CC -1- SUBUNIT: Homodimer (By similarity).  
 CC -1- SUBCELLULAR LOCATION: Cytoplasmic.  
 CC -1- POLYMORPHISM: Was sequenced in many cultivars; Ag-0, Bl-1, Bus-1,  
 CC Cl-0, Cvi-0, Dra-0, Edi-0, Han-0, Hiroshima, In-0, Ita-0, Kas-1,  
 CC Mr-0, Noh-4, Ost-0, Pog-0, Rou-0, Su-0, Ts-1 and ws-0.  
 CC -1- SIMILARITY: BELONGS TO THE GPI FAMILY.  
 CC -----  
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 CC -----  
 CC EMBL; X69195; CAA48940.1; -  
 DR EMBL; AB044948; BAB17635.1; -  
 DR EMBL; AB044949; BAB17636.1; -  
 DR EMBL; AB044950; BAB17637.1; -  
 DR EMBL; AB044951; BAB17638.1; -  
 DR EMBL; AB044952; BAB17639.1; -  
 DR EMBL; AB044953; BAB17640.1; -  
 DR EMBL; AB044954; BAB17641.1; -  
 DR EMBL; AB044955; BAB17642.1; -

DR EMBL; AB044956; BAB17643.1; -  
 DR EMBL; AB044957; BAB17644.1; -  
 DR EMBL; AB044958; BAB17645.1; -  
 DR EMBL; AB044959; BAB17646.1; -  
 DR EMBL; AB044960; BAB17647.1; -  
 DR EMBL; AB044961; BAB17648.1; -  
 DR EMBL; AB044962; BAB17649.1; -  
 DR EMBL; AB044963; BAB17650.1; -  
 DR EMBL; AB044964; BAB17651.1; -  
 DR EMBL; AB044965; BAB17652.1; -  
 DR EMBL; AB044966; BAB17653.1; -  
 DR EMBL; AB044967; BAB17654.1; -  
 DR EMBL; AB07647; BAB10650.1; -  
 DR HSSP; Q9N1E2; IHOX.  
 DR InterPro; IPR001672; G6P\_Isomerase.  
 DR Pfam; PF00342; PGI\_1.  
 DR PRINTS; PR00662; G6PISOMERASE.  
 DR PROSITE; PS00765; P\_GLUCOSE\_ISOMERASE\_1; 1.  
 DR PROSITE; PS00174; P\_GLUCOSE\_ISOMERASE\_2; 1.  
 KW Gluconeogenesis; Glycolysis; Isomerase; Polymorphism.  
 FT ACT\_SITE 392 392  
 FT ACT\_SITE 517 517  
 FT ACT\_SITE 517 517  
 FT VARIANT 3 3  
 FT VARIANT 5 5  
 FT VARIANT 3 3  
 FT VARIANT 36 36  
 FT VARIANT 73 73  
 FT VARIANT 95 95  
 FT VARIANT 99 99  
 FT VARIANT 105 105  
 FT VARIANT 114 114  
 FT VARIANT 119 119  
 FT VARIANT 198 198  
 FT VARIANT 295 295  
 FT VARIANT 355 355  
 FT VARIANT 425 425  
 FT VARIANT 431 431  
 FT VARIANT 432 432  
 FT VARIANT 528 528  
 SQ SEQUENCE 560 AA; 61717 MW; C4F5C7D8FE5F193B CRC64;  
 Query Match 60.3%; Score 41; DB 1; Length 560;  
 Best Local Similarity 61.5%; Pred. No. 12;  
 Matches 8; Conservative 1; Mismatches 4; Indels 0; Gaps 0;  
 Cy 1 KTGAAPAEGRHY 13  
 Db 531 RTGAAPAEGRHY 543  
 RESULT 5  
 ID YL81\_ARCFU STANDARD, PRT; 212 AA.  
 AC YL81\_ARCFU STANDARD, PRT; 212 AA.  
 DT 16-OCT-2001 (Rel. 40, Created)  
 DT 16-OCT-2001 (Rel. 40, Last sequence update)  
 DT 16-OCT-2001 (Rel. 40, Last annotation update)  
 DE Hypothetical protein AR2181.  
 GN AF2181.  
 OS Archaeoglobus fulgidus.  
 OC Archaea; Euryarchaeota; Archaeoglobales;  
 OC Archaeoglobaceae; Archaeoglobus.  
 CC NCB1\_TaxID=2234;  
 [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=VC-16 / DSM 4304 / ATCC 49558;  
 RX MEDLINE=98049343; PubMed=9389475;  
 RA Klank H.-P., Clayton R.A., Tomb J.-F., White O., Nelson K.E.,  
 RA Ketchum K.A., Dodson R.J., Gwinn M., Hickey E.K., Peterson J.D.,  
 RA Richardson D.L., Kerlavage A.R., Graham D.E., Kyprides N.C.,  
 RA Fleischmann R.D., Quackenbush J., Lee N.H., Sutton G.G., Gill S.,  
 RA Kitzies E.F., Dougherty B.A., McKenney K., Adams M.D., Loftus B.,  
 RA Peterson S., Reich C.I., McNeil L.K., Badger J.H., Glodek A., Zhou L.,

Overbeek R., Gocayne J.D., Weisman J.F., McDonald L., Uterback T.,  
 Cotton M.D., Spriggs T., Arlisch P., Kaine B.P., Sykes S.M.,  
 Sadow P.W., D'Andrea K.P., Bowman C., Fujii C., Garland S.A.,  
 Mason T.M., Olsen G.J., Fraser C.M., Smith H.O., Weiss C.R.,  
 Venter J.C.,  
 "The complete genome sequence of the hyperthermophilic, sulphate-  
 reducing archaeon *Archaeoglobus fulgidus*.";  
 Nature 390:364-370(1997).  
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 -----  
 EMBL; AE000954; AAB89076.1; -.  
 PIR; E69522; E69522.  
 TIGR; AF2181; -.  
 Hypothetical protein; Complete proteome.  
 KM SEQUENCE 212 AA; 24115 MW; 1537182512DEBDB CRC64;  
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 Query Match 57.4%; Score 39; DB 1; Length 212;  
 Best Local Similarity 72.7%; Pred. No. 10;  
 Matches 8; Conservative 0; Mismatches 3; Indels 0; Gaps 0;  
 -----  
 QY 3 ACTAPTAGNYS 13  
 Db 132 AGAALAGNYS 142  
 -----  
 RESULT 6  
 CDSA\_MYCTU STANDARD; PRT; 306 AA.  
 ID CDSA\_MYCTU  
 AC 010607;  
 DT 01-OCT-1996 (Rel. 34, Created)  
 DT 01-OCT-1996 (Rel. 34, Last sequence update)  
 DT 28-FEB-2003 (Rel. 41, Last annotation update)  
 DE Phosphatidate cytidyltransferase (EC 2.7.7.41) (CDP-diacylglycerol  
 synthetase) (CDP-diacylglyceride pyrophosphorylase) (CDP-diacylglycerol  
 synthase) (CDP-DG synthetase).  
 GN CDSA OR RV2881C OR MT2948 OR MTCY274.12C.  
 OS Mycobacterium tuberculosis.  
 OC Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;  
 OC Corynebacteriaceae; Mycobacteriaceae; Mycobacterium.  
 CC NCB1\_TaxId=1773;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=H37RV;  
 RX MEDLINE=98295987; PubMed=9634230;  
 RA Cole S.T., Broesch R., Parkhill J., Garnier T., Churcher C., Harris D.,  
 Gordon S.V., Eigleman K., Gas S., Barry C.E. III, Tekala F.,  
 Badcock K., Basham D., Brown D., Chillingworth T., Connor R.,  
 Davies R., Devlin K., Feltwell T., Gentles S., Hamlin N., Holroyd S.,  
 Hornsby T., Jaseki K., Kroch A., McLean J., Moule S., Murphy L.,  
 Oliver S., Osborne J., Quail M.A., Rajandream M.A., Rogers J.,  
 Rutter S., Seeger K., Skelton S., Squares S., Squares K.,  
 Sulten J.E., Taylor K., Whitehead S., Barrell B.G.;  
 RA "Deciphering the biology of *Mycobacterium tuberculosis* from the  
 RT complete genome sequence.";  
 RL Nature 393:537-544(1998).  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=CDC 1551 / Oshkosh;  
 RA Fleischmann R.D., Alland D., Eisen J.A., Carpenter L., White O.,  
 Peterson J., DeBoy R., Dodson R., Gwinn M.L., Haft D., Hickey E.,  
 Kolonay J.F., Nelson W.C., Umayam L.A., Ermolaeva M.D., Salzberg S.L.,  
 Delcher A., Uterback T., Weidman J., Khouri H., Gill J., Mikula A.,  
 Bishai W.;  
 RA "Whole genome comparison of *Mycobacterium tuberculosis* clinical and  
 RT laboratory strains.";

Submitted (Apr-2001) to the EMBL/GenBank/DBJ databases.  
 CC -1- CATALYTIC ACTIVITY: CTP + phosphatidate = diphosphate + CDP-  
 CC diacylglycerol.  
 CC -1- PATHWAY: Phospholipid biosynthesis.  
 CC -1- SUBCELLULAR LOCATION: Integral membrane protein (Potential).  
 CC -1- SIMILARITY: BELONGS TO THE CDS FAMILY.  
 -----  
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 -----  
 EMBL; Z74024; CA98357.1; -.  
 PIR; D70924; D70924.  
 TIGR; MT2948; -.  
 DR Tuberculin; RV2881C; -.  
 DR InterPro: IPR000374; PCTransf.  
 DR Pfam: PF01148; CTP\_transf\_1; 1.  
 DR PROSITE: PS01315; CDS, 1.  
 KW Transferase; Nucleotidyltransferase, Phospholipid biosynthesis;  
 KM Transmembrane; Complete proteome.  
 FT TRANSMEM 36 56 POTENTIAL.  
 FT TRANSMEM 82 102 POTENTIAL.  
 FT TRANSMEM 103 123 POTENTIAL.  
 FT TRANSMEM 151 171 POTENTIAL.  
 FT TRANSMEM 180 200 POTENTIAL.  
 FT TRANSMEM 218 238 POTENTIAL.  
 FT TRANSMEM 241 261 POTENTIAL.  
 FT TRANSMEM 285 305 POTENTIAL.  
 SQ SEQUENCE 306 AA; 32035 MW; 8FA81A108035099F CRC64;  
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 Query Match 57.4%; Score 39; DB 1; Length 306;  
 Best Local Similarity 63.6%; Pred. No. 15;  
 Matches 7; Conservative 1; Mismatches 3; Indels 0; Gaps 0;  
 -----  
 QY 2 TAGAPTAGNY 12  
 Db 135 TTGAPSPGNY 145  
 -----  
 RESULT 7  
 A85B\_MYCSC STANDARD; PRT; 330 AA.  
 ID A85B\_MYCSC  
 AC 050397;  
 DT 16-OCT-2001 (Rel. 40, Created)  
 DT 16-OCT-2001 (Rel. 40, Last sequence update)  
 DT 16-OCT-2001 (Rel. 40, Last annotation update)  
 DE Antigen 85-B precursor (85B) (Extracellular alpha-antigen) (Antigen 85  
 complex B) (Ag85B) (Mycolyl transferase 85B) (EC 2.3.1.-)  
 DE (Fibronectin-binding protein B).  
 GN FBPB.  
 OS Mycobacterium scrofulaceum.  
 OC Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;  
 OC Corynebacteriaceae; Mycobacteriaceae; Mycobacterium.  
 CC NCB1\_TaxId=1783;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=ATCC 19981;  
 RX MEDLINE=9433707; PubMed=8047837;  
 RA Takano M., Ohara N., Mizuno A., Yamada T.;  
 RT "Cloning, sequencing and expression in *Escherichia coli* of the gene  
 RT for alpha antigen from *Mycobacterium scrofulaceum*.";  
 RL Scand. J. Immunol. 40:165-170(1994).  
 CC -1- FUNCTION: PROTEINS OF THE ANTIGEN 85 COMPLEX ARE RESPONSIBLE FOR  
 CC THE HIGH AFFINITY OF MYCOBACTERIA TO FIBRONECTIN. POSSESSES A  
 CC MYCOYLTRANSFERASE ACTIVITY REQUIRED FOR THE BIOGENESIS OF  
 CC TREHALOSE DIMYCOLATE (CORD FACTOR), A DOMINANT STRUCTURE NECESSARY  
 CC FOR MAINTAINING CELL WALL INTEGRITY (BY SIMILARITY).  
 CC -1- SUBCELLULAR LOCATION: Secreted.

CC -1- SIMILARITY: TO OTHER MYCOBACTERIUM A85 ANTIGENS AND TO THE  
 CC N-TERMINAL OF C.GLUTAMICUM PSI PROTEIN.  
 CC -----  
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 CC -----  
 CC EMBL; D26187; BAA05332.1; -.  
 CC DR HSSP; P31953; 1DQY.  
 CC DR InterPro; IPR000801; Esterase\_put.  
 CC DR Pfam; PF00756; Esterase; 1.  
 CC KW Transferrase; Acyltransferase; Antigen; Signal.  
 CC FT SIGNAL 1 40 BY SIMILARITY.  
 CC FT CHAIN 1 330 ANTIGEN 85-B.  
 CC FT ACT SITE 166 166 BY SIMILARITY.  
 CC FT ACT SITE 270 270 BY SIMILARITY.  
 CC FT ACT SITE 302 302 BY SIMILARITY.  
 CC SQ SEQUENCE 330 AA; 34943 MW; 09D6E04B5E9ED221 CRC64;  
 CC -----  
 CC Query Match 57.4%; Score 39; DB 1; Length 330;  
 CC Best Local Similarity 72.7%; Pred. No. 16;  
 CC Matches 8; Conservative 1; Mismatches 2; Indels 0; Gaps 0;  
 CC -----  
 CC QY 3 AGTAPTAGNYS 13  
 CC DB 32 AGGAPTAGAFS 42  
 CC -----  
 CC RESULT 8  
 CC MP92\_POAPR STANDARD; PRT; 333 AA.  
 CC ID MP92\_POAPR STANDARD; PRT; 333 AA.  
 CC AC P22285;  
 CC DT 01-AUG-1991 (Rel. 19, Created)  
 CC DT 01-AUG-1991 (Rel. 19, Last sequence update)  
 CC DT 01-NOV-1997 (Rel. 35, Last annotation update)  
 CC DE Pollen allergen KBG 41 precursor (Pollen allergen Poa p 9) (Poa p IX).  
 CC OS Pollen pratinensis (Kentucky bluegrass).  
 CC CC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 CC CC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooidae;  
 CC CC Poaceae; Poa.  
 CC CC NCBI\_TaxID=4545;  
 CC CC [1]  
 CC CC SEQUENCE FROM N.A.  
 CC CC TISSUE=Pollen;  
 CC CC MEDLINE=91093232; PubMed=1702432;  
 CC RA Silvanovich A., Astwood J., Zhang L., Olsen E., Kisil F.T.,  
 CC RA Sehon A.H., Mohapatra S.S., Hill R.D.;  
 CC RT "Nucleotide sequence analysis of three cDNAs coding for Poa p IX  
 CC RT isoallergens of Kentucky bluegrass pollen.";  
 CC RL J. Biol. Chem. 266:1204-1210(1991).  
 CC [2]  
 CC CHARACTERIZATION.  
 CC RP MEDLINE=91268549; PubMed=2051020;  
 CC RA Olsen E., Zhang L., Hill R.D., Kisil F.T., Sehon A.H., Mohapatra S.S.;  
 CC RT "Identification and characterization of the Poa p IX group of basic  
 CC RT allergens of Kentucky bluegrass pollen.";  
 CC RL J. Immunol. 147:205-211(1991).  
 CC CC -1- TISSUE SPECIFICITY: POLLEN.  
 CC CC -1- MISCELLANEOUS: ITS C-TERMINUS MIGHT BE MEMBRANE-ASSOCIATED.  
 CC CC -1- SIMILARITY: BELONGS TO THE POA P IX/PHL P VI FAMILY OF ALLERGENS.  
 CC -----  
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 CC -----

DR EMBL; M38343; AAA63456.1; -.  
 DR PIR; A39098; A39098.  
 DR InterPro; IPR001778; POA\_allergenc.  
 DR InterPro; IPR002914; POA\_allergenn.  
 DR Pfam; PF01620; Pollen\_allerg\_2; 1.  
 DR PRINTS; PR00833; POAALLERGEN.  
 CC KW Allergen; Signal; Multigene family; Repeat.  
 CC FT SIGNAL 1 23 POTENTIAL.  
 CC FT CHAIN 24 333 POLLEN ALLERGEN KBG 41.  
 CC FT DOMAIN 309 332 2 X 12 AA TANDEM REPEATS.  
 CC FT REPEAT 309 320 1.  
 CC FT REPEAT 321 332 2.  
 CC SQ SEQUENCE 333 AA; 32661 MW; 1FA48168C1134CA0 CRC64;  
 CC -----  
 CC Query Match 57.4%; Score 39; DB 1; Length 333;  
 CC Best Local Similarity 58.3%; Pred. No. 16;  
 CC Matches 7; Conservative 0; Mismatches 5; Indels 0; Gaps 0;  
 CC -----  
 CC QY 1 KTGAATPTAGGY 12  
 CC DB 320 KTGAATPTAGGY 331  
 CC -----  
 CC RESULT 9  
 CC REV\_SIVCZ STANDARD; PRT; 124 AA.  
 CC ID REV\_SIVCZ STANDARD; PRT; 124 AA.  
 CC AC P17280;  
 CC DT 01-AUG-1990 (Rel. 15, Created)  
 CC DT 01-AUG-1990 (Rel. 15, Last sequence update)  
 CC DT 28-FEB-2003 (Rel. 41, Last annotation update)  
 CC DE REV protein (Anti-repression transactivator protein) (ART/TRS).  
 CC GN REV.  
 CC OS Chimpanzee immunodeficiency virus (SIV(Cpz)) (CIV).  
 CC OS Viruses; Retrodeltaviruses; Retroviridae; Lentiviruses.  
 CC CC NCBI\_TaxID=11723;  
 CC CC [1]  
 CC CC SEQUENCE FROM N.A.  
 CC CC MEDLINE=90259077; PubMed=2188136;  
 CC RA Hueb T., Cheynier R., Meyers A., Roelants G., Wain-Hobson S.;  
 CC RT "Genetic organization of a chimpanzee lentivirus related to HIV-1.";  
 CC RL Nature 345:356-359(1990).  
 CC CC -1- FUNCTION: REV APPEARS TO ACT POST-TRANSCRIPTIONALLY TO RELIEVE  
 CC CC NEGATIVE REGRESSION OF GAG AND ENV PRODUCTION.  
 CC CC -1- SUBCELLULAR LOCATION: Nuclear; accumulates in the nucleoli.  
 CC CC -1- PTM: PHOSPHOPROTEIN WHOSE STATE OF PHOSPHORYLATION IS MEDIATED  
 CC CC BY A SPECIFIC SERINE KINASE ACTIVITY PRESENT IN THE NUCLEUS.  
 CC -----  
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 CC -----  
 CC EMBL; X52154; CAA36405.1; -.  
 CC DR PIR; S09988; VKLJST.  
 CC DR HIT; X52154; REVSCPZ.  
 CC DR InterPro; IPR000625; REV\_protein.  
 CC DR Pfam; PF00424; REV; 1.  
 CC KW Transcription regulation; AIDS; Phosphorylation; Nuclear protein.  
 CC SQ SEQUENCE 124 AA; 13701 MW; F5877D1BDFF65A782 CRC64;  
 CC -----  
 CC Query Match 55.9%; Score 38; DB 1; Length 124;  
 CC Best Local Similarity 58.3%; Pred. No. 9;  
 CC Matches 7; Conservative 0; Mismatches 5; Indels 0; Gaps 0;  
 CC -----  
 CC QY 2 TAGTAPTAGNYS 13  
 CC DB 105 TGTIVPAGNYS 116  
 CC -----  
 CC RESULT 10

RLA0\_CHERU STANDARD; PRT; 321 AA.  
 ID\_RLA0\_CHERU  
 AC P29764;  
 DT 01-APR-1993 (Rel. 25, Created)  
 DT 01-APR-1993 (Rel. 25, Last sequence update)  
 DT 01-OCT-1996 (Rel. 34, Last annotation update)  
 DE 60S acidic ribosomal protein P0 (light-induced 34 kDa protein).  
 OS Chenopodium rubrum (Red goosefoot) (Pigweed).  
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;  
 OC Caryophyllales; Caryophyllales; Chenopodiaceae; Chenopodium.  
 NCBI\_TaxID=3560;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RA Kalenhoff R., Richter G.;  
 RL Submitted (MAY-1989) to the EMBL/GenBank/DBJ databases.  
 CC -1- FUNCTION: RIBOSOMAL PROTEIN P0 IS THE FUNCTIONAL EQUIVALENT  
 CC OF E.COLI PROTEIN L10.  
 CC -1- SUBUNIT: P0 FORMS A PENTAMERIC COMPLEX BY INTERACTION WITH  
 CC DIMERS OF P1 AND P2 (BY SIMILARITY).  
 CC -1- SIMILARITY: BELONGS TO THE L10P FAMILY OF RIBOSOMAL PROTEINS.  
 CC -----  
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 CC -----  
 CC EMBL; X15206; CAA3276.1; -  
 CC DR PIR; S21519; RSUBP0.  
 CC DR InterPro; IPR001813; 60S\_ribosomal.  
 CC DR InterPro; IPR001790; Ribosomal\_L10.  
 CC DR Pfam; PF00428; 60S\_ribosomal\_1.  
 CC DR Pfam; PF00466; Ribosomal\_L10; 1.  
 CC DR Ribosomal protein; phosphorylation.  
 CC KW SEQUENCE 321 AA; 34351 MW; 3A3333FC86EC0B2 CRC64;  
 SQ  
 Query Match 55.9%; Score 38; DB 1; Length 321;  
 Best Local Similarity 77.8%; Pred. No. 23;  
 Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;  
 QY 2 TAGTAPTGT 10  
 DB 284 SAGTAPTGT 292

RA Bortiss R., Bourcier L., Brans A., Braun M., Brignell S.C., Bron S.,  
 RA Brouillet S., Brusch C.V., Caldwell B., Capuano V., Carter N.M.,  
 RA Choi S.K., Codani J.J., Comerton I.F., Cummings N.J., Daniel R.A.,  
 RA Denton F., Devine K.M., Dusterhoft A., Ehrlich S.D., Emerson P.T.,  
 RA Entian K.D., Errington J., Fabret C., Ferrari E., Foulger D.,  
 RA Fritz C., Fujita M., Fujita Y., Fuma S., Galizzi A., Galleron N.,  
 RA Ghim S.Y., Glaser P., Goffeau A., Gollightly E.J., Gradi G.,  
 RA Hilbert H., Holsappel S., Hosono S., Hullo M.F., Itaya M., Jones L.,  
 RA Joris B., Karamata D., Kasahara Y., Klaerr-Blanchard M., Klein C.,  
 RA Kobayashi Y., Koeltter P., Koningsreim G., Krogh S., Kumano M.,  
 RA Kurita K., Lapidus A., Lardinois S., Lauber J., Lazarevic V.,  
 RA Lee S.M., Levine A., Liu H., Masuda S., Mauel C., Medigue C.,  
 RA Medina N., Melillo R.P., Mizuno M., Moestl D., Nakai S., Nodack M.,  
 RA Noone D., O'Reilly M., Ogawa K., Ogihara A., Oudega B., Park S.H.,  
 RA Parro V., Pohl T.M., Portelle D., Porwollik S., Prescott A.M.,  
 RA Prescan E., Puig P., Purrelle B., Rapoport G., Rey M., Reynolds S.,  
 RA Rieger M., Rivolta C., Rocha E., Roche B., Rose M., Sadate Y.,  
 RA Sato T., Scanlan E., Schleich S., Schroeter R., Scoffone F.,  
 RA Sekiguchi J., Sekowska A., Seror S.J., Seror P., Shin B.S., Soldo B.,  
 RA Sorokin A., Tacconi E., Takagi T., Takahashi H., Takemura K.,  
 RA Takeuchi M., Tamakoshi A., Tanaka T., Terpestra P., Tognoni A.,  
 RA Toato V., Uchiyama S., Vandenbol M., Vannier F., Vassarotti A.,  
 RA Viari A., Wambut R., Wedler E., Wedler H., Weitzneger T.,  
 RA Winters P., Wipat A., Yamamoto H., Yamane K., Yasumoto K., Yata K.,  
 RA Yoshida K., Yoshikawa H.F., Zumbstein E., Yoshikawa H., Danchin A.,  
 RT "The complete genome sequence of the Gram-positive bacterium *Bacillus*  
 RT subtilis".  
 RL Nature 390:249-256(1997).  
 RN [3]  
 RP SEQUENCE OF 1-57 FROM N.A.  
 RC STRAIN=168;  
 RX MEDLINE=95020537; PubMed=7934828;  
 RA Glaser P., Kunst F., Arnard M., Coudart M.P., Gonzales W.,  
 RA Hullo M.F., Ionescu M., Lubochinsky B., Marcelino L., Moszer I.,  
 RA Presecan E., Santana M., Schneider E., Schweizer J., Verres A.,  
 RA Rapoport G., Danchin A.;  
 RT "Bacillus subtilis genome project: cloning and sequencing of the 97  
 RT kb region from 325 degrees to 333 degrees".  
 RL Mol. Microbiol. 10:371-384(1993).  
 RN [4]  
 RP SEQUENCE OF 1-9.  
 RC STRAIN=168; IS58;  
 RX MEDLINE=97443988; PubMed=9298659;  
 RA Antelmann H., Bernhardt J., Schmid R., Mach H., Voelker U.,  
 RA Hecker M.;  
 RT "First steps from a two-dimensional protein index towards a response-  
 RT regulation map for *Bacillus subtilis*.";  
 RL Electrophoresis 18:1451-1463(1997).  
 CC -1- FUNCTION: Acts on leucine, isoleucine and valine (By similarity).  
 CC -1- CATALYTIC ACTIVITY: L-leucine + 2-oxoglutarate = 4-methyl-2-  
 CC oxopentanoate + L-glutamate.  
 CC -1- COFACTOR: Pyridoxal phosphate.  
 CC -1- PATHWAY: Valine and isoleucine biosynthesis.  
 CC -1- SIMILARITY: BELONGS TO CLASS-IV OF PYRIDOXAL-PHOSPHATE-DEPENDENT  
 CC AMINOTRANSFERASES.  
 CC -----  
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 CC -----  
 CC EMBL; Z49992; CAA90289.1; -  
 CC DR EMBL; Z59123; CAA15881.1; -  
 CC DR EMBL; X73124; CAA51556.1; -  
 CC DR PIR; S57763; S57763.  
 CC DR HSSP; P00510; IAG3.  
 CC Subtilist; BG10546; ywaA.  
 DR InterPro; IPR001544; Aminotran\_4.  
 DR InterPro; IPR005786; B\_amino\_transit.

DR Pfam; PF01063; aminotran\_4; 1.  
DR ProDom; PD001961; Aminotran\_4; 1.  
DR TIGRfams; TIGR01123; Iive II; 1.  
DR PROSITE; PS00770; AA TRANSFER CLASS 4; 1.  
KW Transferase; Aminotransferase; Branched-chain amino acid biosynthesis;  
KW Pyridoxal phosphate; Complete proteome.  
FT INIT MET 0  
FT BINDING 196 196 PYRIDOXAL PHOSPHATE (BY SIMILARITY).  
SQ SEQUENCE 362 AA; 40191 MW; FFB681ASFDC7057 CRC64;  
  
Query Match 55.9%; Score 38; DB 1; Length 362;  
Best Local Similarity 70.0%; Pred. No. 26;  
Matches 7; Conservative 1; Mismatches 2; Indels 0; Gaps 0;  
  
QY 4 GTAPTAGNYS 13  
DB 193 GNATKAGNYA 202  
  
RESULT 12  
VSGP\_EBOEC STANDARD; PRT; 364 AA.  
AC P87670;  
DT 16-OCT-2001 (Rel. 40, Created)  
DT 16-OCT-2001 (Rel. 40, Last sequence update)  
DT 16-OCT-2001 (Rel. 40, Last annotation update)  
DE Small/secreted glycoprotein precursor (SGP).  
GN GP.  
OS Ebola virus (strain Eckron-76) (Ebo).  
OC Viruses; ssRNA negative-strand viruses; Mononegavirales; Filoviridae;  
OC Ebola-like viruses.  
OX NCBI\_TaxID=129000;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=97329084; PubMed=9185597;  
RA Volchkov V., Volchkova V., Eckel C., Klenk H.D., Bouloy M.,  
Leguenno B., Feldmann H.;  
RT "Emergence of subtype Zaire Ebola virus in Gabon.";  
Virology 232:139-144(1997).  
CC -1- SUBCELLULAR LOCATION: Secreted.  
CC -1- MISCELLANEOUS: THIS PROTEIN IS SYNTHESIZED WHEN NO RNA-EDITING  
TAKES PLACE DURING TRANSCRIPTION.  
CC -1- SIMILARITY: BELONGS TO THE FILOVIRUSES GLYCOPROTEIN FAMILY.  
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-----  
CC EMBL; U81161; AAC57993.1; -  
DR InterPro; IPR002561; Filo\_glycop.  
DR Pfam; PF01611; Filo\_glycop; 1.  
KW Glycoprotein; Signal.  
FT CHAIN 1 32  
FT SIGNAL 1 32  
FT CARBOHYD 33 364  
FT CARBOHYD 40 40  
FT CARBOHYD 204 204  
FT CARBOHYD 228 228  
FT CARBOHYD 238 238  
FT CARBOHYD 257 257  
FT CARBOHYD 268 268  
SQ SEQUENCE 364 AA; 41202 MW; 5D034F8DA5EE2695 CRC64;  
  
Query Match 55.9%; Score 38; DB 1; Length 364;  
Best Local Similarity 46.2%; Pred. No. 26;  
Matches 6; Conservative 4; Mismatches 3; Indels 0; Gaps 0;  
  
QY 1 KTACTAPTAGNYS 13  
DB 140 KVSQTGPAGDFA 152

RESULT 13  
VSGP\_EBOG4 STANDARD; PRT; 364 AA.  
ID O11458;  
DT 16-OCT-2001 (Rel. 40, Created)  
DT 16-OCT-2001 (Rel. 40, Last sequence update)  
DT 16-OCT-2001 (Rel. 40, Last annotation update)  
DE Small/secreted glycoprotein precursor (SGP).  
GN GP.  
OS Ebola virus (strain Gabon-94) (Ebo).  
OC Viruses; ssRNA negative-strand viruses; Mononegavirales; Filoviridae;  
OC Ebola-like viruses.  
OX NCBI\_TaxID=128947;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=97329084; PubMed=9185597;  
RA Volchkov V., Volchkova V., Eckel C., Klenk H.D., Bouloy M.,  
Leguenno B., Feldmann H.;  
RT "Emergence of subtype Zaire Ebola virus in Gabon.";  
Virology 232:139-144(1997).  
CC -1- SUBCELLULAR LOCATION: Secreted.  
CC -1- SIMILARITY: BELONGS TO THE FILOVIRUSES GLYCOPROTEIN FAMILY.  
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-----  
CC EMBL; U77384; AAC57990.1; -  
DR InterPro; IPR002561; Filo\_glycop.  
DR Pfam; PF01611; Filo\_glycop; 1.  
KW Glycoprotein; Signal.  
FT CHAIN 1 32  
FT SIGNAL 1 32  
FT CARBOHYD 33 364  
FT CARBOHYD 40 40  
FT CARBOHYD 204 204  
FT CARBOHYD 228 228  
FT CARBOHYD 238 238  
FT CARBOHYD 257 257  
FT CARBOHYD 268 268  
SQ SEQUENCE 364 AA; 41218 MW; 7B46B128FA3B82A5 CRC64;  
  
Query Match 55.9%; Score 38; DB 1; Length 364;  
Best Local Similarity 46.2%; Pred. No. 26;  
Matches 6; Conservative 4; Mismatches 3; Indels 0; Gaps 0;  
  
QY 1 KTACTAPTAGNYS 13  
DB 140 KVSQTGPAGDFA 152  
  
RESULT 14  
VSGP\_EBOZM STANDARD; PRT; 364 AA.  
AC Q66819; O12421; O12717; Q66801; Q9YMG3;  
DT 16-OCT-2001 (Rel. 40, Created)  
DT 16-OCT-2001 (Rel. 40, Last sequence update)  
DT 16-OCT-2001 (Rel. 40, Last annotation update)  
DE Small/secreted glycoprotein precursor (SGP).  
GN GP.  
OS Ebola virus (strain Zaire Mayinga) (Ebo), and  
OS Ebola virus (strain Zaire-95) (Ebo).  
OC Viruses; ssRNA negative-strand viruses; Mononegavirales; Filoviridae;  
OC Ebola-like viruses.  
OX NCBI\_TaxID=128952, 128951;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=Zaire Mayinga;



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OM protein - protein search, using SW model

Run on: February 6, 2004, 11:37:31; Search time 35 Seconds  
(without alignments)  
95.848 Million cell updates/sec

Title: US-09-618-577-28

Perfect score: 68  
Sequence: 1 KTAGTAPTAGNYS 13

Scoring table: BLOSUM62  
Gapop 10.0, Gapext 0.5

Searched: 830525 seqs, 258052604 residues

Total number of hits satisfying chosen parameters: 830525

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database:

SPTREMBL\_23:\*

- 1: sp\_archaea:\*
- 2: sp\_bacteria:\*
- 3: sp\_fungi:\*
- 4: sp\_human:\*
- 5: sp\_invertebrate:\*
- 6: sp\_mammal:\*
- 7: sp\_mhc:\*
- 8: sp\_organelle:\*
- 9: sp\_phage:\*
- 10: sp\_plant:\*
- 11: sp\_protist:\*
- 12: sp\_virus:\*
- 13: sp\_vertebrate:\*
- 14: sp\_unclassified:\*
- 15: sp\_virus:\*
- 16: sp\_bacterioph:\*
- 17: sp\_archaeap:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	68	100.0	170	2	Q93V20
2	48	70.6	135	2	Q47120
3	47	69.1	134	2	Q47122
4	47	69.1	167	2	Q93G69
5	46	67.6	142	2	Q47124
6	43	63.2	217	1	Q97782
7	42	61.8	82	2	Q8GAD2
8	42	61.8	358	16	Q9KAY0
9	41	60.3	179	10	Q39G95
10	41	60.3	181	2	Q9AG87
11	41	60.3	249	5	Q8T306
12	41	60.3	313	10	Q04828
13	41	60.3	560	10	Q94UT1
14	41	60.3	573	5	Q8WS24
15	41	60.3	672	11	Q8CG10
16	41	60.3	685	11	Q8C1S1

17	41	60.3	795	11	Q9DBY0	Q9dby0 mus musculus
18	41	60.3	965	5	Q9VAM5	Q9vams drosophila
19	41	60.3	1403	5	Q9NHM6	Q9nhm6 drosophila
20	41	60.3	1403	5	Q8IMM4	Q8imm4 drosophila
21	40	58.8	346	10	Q82525	Q82525 arabidopsis
22	40	58.8	362	10	Q9FMG1	Q9fmgl arabidopsis
23	40	58.8	469	12	Q8B198	Q8b198 influenza a
24	40	58.8	469	12	Q8B197	Q8b197 influenza a
25	40	58.8	506	11	Q8K383	Q8k383 mus musculus
26	40	58.8	787	10	Q9FGC1	Q9fgcl arabidopsis
27	40	58.8	792	5	Q23115	Q23115 caenorhabditis
28	40	58.8	956	10	Q8RWH3	Q8rwh3 arabidopsis
29	40	58.8	1275	4	Q9UQ36	Q9uq36 homo sapien
30	40	58.8	1783	4	Q15038	Q15038 homo sapien
31	40	58.8	1791	4	Q60382	Q60382 homo sapien
32	40	58.8	2607	11	Q8BRT8	Q8brt8 mus musculus
33	40	58.8	2752	4	Q9UQ35	Q9uq35 homo sapien
34	39	57.4	144	9	Q9G0P9	Q9g0p9 roseophage
35	39	57.4	234	2	Q8GF82	Q8gfs2 citrobacter
36	39	57.4	256	10	Q24568	Q24568 zea mays
37	39	57.4	285	10	Q8H367	Q8h367 oryza sativ
38	39	57.4	426	10	Q8S5V5	Q8s5v5 oryza sativ
39	39	57.4	724	5	Q9GTR8	Q9gtr8 hydra attenu
40	39	57.4	890	10	Q8W5R6	Q8w5r6 arabidopsis
41	39	57.4	909	10	Q9X103	Q9x103 arabidopsis
42	39	57.4	928	16	Q8PEU8	Q8peu8 xanthomonas
43	39	57.4	1216	11	Q8BUP1	Q8bup1 mus musculus
44	38	56.6	241	12	Q89247	Q89247 marek's dis
45	38	55.9	67	2	Q9X6L7	Q9x6l7 klebsiella

#### ALIGNMENTS

##### RESULT 1

Q93V20; PRELIMINARY; PRT; 170 AA.

AC Q93V20;  
DT 01-DEC-2001 (TREMBlrel. 19, Created)  
DT 01-DEC-2001 (TREMBlrel. 19, Last sequence update)  
DT 01-MAR-2003 (TREMBlrel. 23, Last annotation update)  
DE Colonization factor antigen 1.  
OS Escherichia coli.  
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;  
OC Enterobacteriaceae; Escherichia.  
OX NCBI\_TaxID=562;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=94207144; PubMed=8155840;  
RA Zhang Z., Li S., Huang C.;  
RT "Sequence analysis of the colonization factor antigen 1 gene of EPEC  
and observation of CF/A1 recombinant clone with electron microscopy.";  
RL Chin. J. Biotechnol. 9:57-61 (1993).  
DR EMBL; S73191; AAB30543.1; -;  
DR Pfam; PF04449; Fimbrin CSI; 1.  
SQ SEQUENCE 170 AA; 17433 MW; 894347E2F43E56B4 CRC64;

Query Match 100.0%; Score 68; DB 2; Length 170;  
Best Local Similarity 100.0%; Pred. No. 0.00054;  
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KTAGTAPTAGNYS 13  
DB 147 KTAGTAPTAGNYS 159

##### RESULT 2

Q47120; PRELIMINARY; PRT; 135 AA.  
AC Q47120;  
DT 01-NOV-1996 (TREMBlrel. 01, Created)  
DT 01-NOV-1996 (TREMBlrel. 01, Last sequence update)  
DT 01-DEC-2001 (TREMBlrel. 19, Last annotation update)

```

DE CsaA protein (Fragment).
GN CSAB.
OS Escherichia coli.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OC Enterobacteriaceae; Escherichia.
OX NCBI_TaxID=562;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=E20738A;
RA Gastra W., Kusters J.G., Van Dijk L.;
RT "The major subunit gene for Csa4 fimbriae is duplicated in the CS14
RT fimbrial operon.";
RL Submitted (Apr-1996) to the EMBL/GenBank/DBJ databases.
DR EMBL; X97495; CAA66126.1; -.
FT NON_TER 1 135
SQ SEQUENCE 135 AA; 14277 MW; 88964DB09C944B6F CRC64;

Query Match 70.6%; Score 48; DB 2; Length 135;
Best Local Similarity 81.8%; Pred. No. 1.3;
Matches 9; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 TAGTAPTAGNY 12
DB 113 TGTATPAGNY 123

RESULT 3
Q47122 PRELIMINARY; PRT; 134 AA.
ID Q47122;
AC Q47122;
DT 01-NOV-1996 (TREMBlrel. 01, Created)
DT 01-NOV-1996 (TREMBlrel. 01, Last sequence update)
DT 01-DEC-2001 (TREMBlrel. 19, Last annotation update)
DE Csa4 protein (Fragment).
GN CSFA.
OS Escherichia coli.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OC Enterobacteriaceae; Escherichia.
OX NCBI_TaxID=562;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=9b1373;
RA Gastra W., Kusters J.G., Van Dijk L.;
RT "The major subunit gene for Csa4 fimbriae is duplicated in the CS14
RT fimbrial operon.";
RL Submitted (Apr-1996) to the EMBL/GenBank/DBJ databases.
DR EMBL; X97493; CAA66124.1; -.
FT NON_TER 1 134
SQ SEQUENCE 134 AA; 13916 MW; 3EEFFDC5861396A4 CRC64;

Query Match 69.1%; Score 47; DB 2; Length 134;
Best Local Similarity 75.0%; Pred. No. 1.9;
Matches 9; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2 TAGTAPTAGNY 13
DB 112 TTAQAPTAGNY 123

RESULT 4
Q93G69 PRELIMINARY; PRT; 167 AA.
ID Q93G69;
AC Q93G69;
DT 01-DEC-2001 (TREMBlrel. 19, Created)
DT 01-DEC-2001 (TREMBlrel. 19, Last sequence update)
DT 01-MAR-2003 (TREMBlrel. 23, Last annotation update)
DE CS4 major fimbriae subunit CsaB.
GN CSAB.
OS Escherichia coli.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OC Enterobacteriaceae; Escherichia.

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OX NCBI_TaxID=562;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=E1181A;
RA Altboum Z.D., Levine M.M., Galen J.E., Barry E.M.;
RT "Isolation and characterization of EPEC CS4 fimbriae encoding genes,
RT and their expression in Shigella flexneri 2a guaba strain CVD 1204.";
RL Submitted (Aug-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF296132; AAK97135.1; -.
FT Pfam; PF04449; fimbrial_CS1.1.
SQ SEQUENCE 167 AA; 17344 MW; 94C7822A7C23A5A CRC64;

Query Match 69.1%; Score 47; DB 2; Length 167;
Best Local Similarity 75.0%; Pred. No. 2.4;
Matches 9; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2 TAGTAPTAGNY 13
DB 145 TTAQAPTAGNY 156

RESULT 5
Q47124 PRELIMINARY; PRT; 142 AA.
ID Q47124;
AC Q47124;
DT 01-NOV-1996 (TREMBlrel. 01, Created)
DT 01-NOV-1996 (TREMBlrel. 01, Last sequence update)
DT 01-MAR-2003 (TREMBlrel. 23, Last annotation update)
DE Csa42 protein (Fragment).
GN CSUA2.
OS Escherichia coli.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OC Enterobacteriaceae; Escherichia.
OX NCBI_TaxID=562;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=E7476A;
RA Gastra W., Kusters J.G., Van Dijk L.;
RT "The major subunit gene for Csa4 fimbriae is duplicated in the CS14
RT fimbrial operon.";
RL Submitted (Apr-1996) to the EMBL/GenBank/DBJ databases.
DR EMBL; X97492; CAA66123.1; -.
DR InterPro; IPR00719; Prot_Kinase.
DR PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
FT NON_TER 1 142
SQ SEQUENCE 142 AA; 14498 MW; 932BF1A7989A4E7D CRC64;

Query Match 67.6%; Score 46; DB 2; Length 142;
Best Local Similarity 72.7%; Pred. No. 3;
Matches 8; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 2 TAGTAPTAGNY 12
DB 113 TSGTAPSAKY 123

RESULT 6
Q977R2 PRELIMINARY; PRT; 217 AA.
ID Q977R2;
AC Q977R2;
DT 01-DEC-2001 (TREMBlrel. 19, Created)
DT 01-DEC-2001 (TREMBlrel. 19, Last sequence update)
DT 01-MAR-2002 (TREMBlrel. 20, Last annotation update)
DE NAD(P)H-flavin oxidoreductase.
OS unclutured crenarchaeote 487.
OC Archaea; Crenarchaeota; environmental samples;
OC marine archaeal group 1.
OX NCBI_TaxID=44557;
RN [1]
RP SEQUENCE FROM N.A.
RA Beja O., Koonin E.V., Aravind L., Taylor L.T., Seitz H., Stein J.L.,
RA Bensen D.C., Feldman R.A., Swanson R.V., Delong E.F.;

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RT "Comparative genomic analysis of coexisting archaeal genetic variants  
 in an Antarctic marine microbial assemblage.";  
 RT Submitted (JUN-2001) to the EMBL/GenBank/DBJ databases.  
 RL EMBL; U40238; AK66808.1; -  
 DR InterPro; IPR000415; Nitroreductase.  
 DR Pfam; PF00881; Nitroreductase; 1.  
 SO SEQUENCE 217 AA; 24624 MW; E22C83B6D4957E67 CRC64;  
 Query Match 63.2%; Score 43; DB 1; Length 217;  
 Best Local Similarity 80.0%; Pred. No. 15;  
 Matches 8; Conservative 1; Mismatches 1; Indels 0; Gaps 0;  
 QY 3 AGTAPTAGNT 12  
 Db 78 ADTAPTAGNF 87  
 RESULT 7  
 ID O8GAD2 PRELIMINARY; PRT; 82 AA.  
 AC O8GAD2;  
 DT 01-MAR-2003 (TREMBlrel. 23, Created)  
 DT 01-MAR-2003 (TREMBlrel. 23, Last sequence update)  
 DT 01-MAR-2003 (TREMBlrel. 23, Last annotation update)  
 DE Putative transposase (Fragment).  
 OS Arthrobacter nicotinovorus.  
 OC Plasmid PAO1.  
 OC Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;  
 OC Micrococcales; Micrococcaceae; Arthrobacter.  
 OX NCBI\_TaxID=29320;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=95115562; PubMed=7815950;  
 RA Grether-Beck S., Iglol G.L., Pust S., Schiltz E., Decker K.,  
 Brandach R.;  
 RT "Structural analysis and molybdenum-dependent expression of the PAO1-  
 encoded nicotinic dehydrogenase genes of Arthrobacter nicotinovorus.";  
 RL Mol. Microbiol. 13:929-936(1994).  
 [2]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=96172783; PubMed=8588735;  
 RA Mendez C., Iglol G., Heminger H., Brandach R.;  
 RT "A PAO1-encoded molybdopterin cofactor gene (moaA) of Arthrobacter  
 nicotinovorus: characterization and site-directed mutagenesis of the  
 encoded protein.";  
 RL Arch. Microbiol. 164:142-151(1995).  
 [3]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=97230479; PubMed=9073580;  
 RA Mendez C., Iglol G.L., Brandach R.;  
 RT "Is1473, a putative insertion sequence identified in the plasmid PAO1  
 from Arthrobacter nicotinovorus: isolation, characterisation and  
 distribution among Arthrobacter species.";  
 RL Plasmid 37:35-41(1997).  
 [4]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=98088982; PubMed=9428706;  
 RA Mendez C., Otto A., Iglol G., Nick P., Brandach R., Schubach B.,  
 Botcher B., Brandach R.;  
 RT "Molybdate-uptake genes and molybdopterin-biosynthesis genes on a  
 bacterial plasmid. Characterization of MoaA as a filament-forming  
 protein with adenosinetriphosphatase activity.";  
 RL Eur. J. Biochem. 250:524-531(1997).  
 [5]  
 RP SEQUENCE FROM N.A.  
 RX Schenk S., Hoelz S., Kraus B., Decker K.;  
 RT "Gene structure and properties of enzymes of the plasmid-encoded  
 nicotine catabolism of Arthrobacter nicotinovorus.";  
 RL J. Mol. Biol. 284:1323-1339(1999).  
 [6]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=21405725; PubMed=11514508;  
 RA Batsch D., Sandu C., Brandach R., Iglol G.L.;

RT "A gene cluster on PAO1 of Arthrobacter nicotinovorus involved in the  
 degradation of the plant alkaloid nicotine: cloning, purification and  
 RT characterization of 2,6-dihydroxypyridine 3-hydroxylase.";  
 RL J. Bacteriol. 183:5262-5267(2001).  
 RN [7]  
 RP SEQUENCE FROM N.A.  
 RA Iglol G.L., Brandach R.;  
 RT "Sequence of the 165 kb Catabolic Plasmid PAO1 from Arthrobacter  
 RT nicotinovorus and identification of a PAO1-dependent Nicotine Uptake  
 RT System.";  
 RL Submitted (SEP-2002) to the EMBL/GenBank/DBJ databases.  
 DR EMBL; AJ507836; CAD4799.1; -  
 KW Plasmid.  
 FT NON TER 1  
 FT NON TER 82  
 SO SEQUENCE 82 AA; 8718 MW; 16317803035C8140 CRC64;  
 Query Match 61.8%; Score 42; DB 2; Length 82;  
 Best Local Similarity 88.9%; Pred. No. 8.2;  
 Matches 8; Conservative 1; Mismatches 0; Indels 0; Gaps 0;  
 QY 2 TAGAPTAG 10  
 Db 44 SAGTAPTAG 52  
 RESULT 8  
 ID O9KAYO PRELIMINARY; PRT; 358 AA.  
 AC O9KAYO;  
 DT 01-OCT-2000 (TREMBlrel. 15, Created)  
 DT 01-OCT-2000 (TREMBlrel. 15, Last sequence update)  
 DT 01-OCT-2000 (TREMBlrel. 22, Last annotation update)  
 DE Branched-chain amino acid aminotransferase (BC 2.6.1.42).  
 GN BCAT OR BH2156.  
 OS Bacillus halodurans.  
 OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.  
 OX NCBI\_TaxID=8665;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=C-125 / JCM 9153;  
 RX MEDLINE=20512582; PubMed=11058132;  
 RA Takami H., Nakasone K., Takaki Y., Maeno G., Sasaki R., Maeni N.,  
 RA Fuji F., Hirama C., Nakamura Y., Ogasawara N., Kuhara S.,  
 Horikoshi K.;  
 RT "Complete genome sequence of the alkaliphilic bacterium Bacillus  
 RT halodurans and genomic sequence comparison with Bacillus subtilis.";  
 RL Nucleic Acids Res. 28:4317-4331(2000).  
 DR EMBL; AP001514; BAB05875.1; -  
 DR HSSP; P00510; 1A3G.  
 DR InterPro; IPR001544; Aminotran\_4.  
 DR InterPro; IPR005786; B\_aminotransf.  
 DR Pfam; PF01063; aminotran\_4; 1.  
 DR ProDom; PD001961; Aminotran\_4; 1.  
 DR TIGRFAMs; TIGR01123; 11VE II; 1.  
 DR PROSITE; PS00770; AA\_TRANSFER CLASS 4; 1.  
 KW Transferrase; Aminotransferase; Complete proteome.  
 SO SEQUENCE 358 AA; 40658 MW; B25FFB62BECF9001 CRC64;  
 Query Match 61.8%; Score 42; DB 16; Length 358;  
 Best Local Similarity 80.0%; Pred. No. 39;  
 Matches 8; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
 QY 4 GTAPTAGNTS 13  
 Db 194 GTATGTGNTS 203  
 RESULT 9  
 ID Q39995 PRELIMINARY; PRT; 179 AA.  
 AC Q39995;  
 DT 01-NOV-1996 (TREMBlrel. 01, Created)

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DT 01-NOV-1996 (TREMBlrel. 01, Last sequence update)
DT 01-OCT-2002 (TREMBlrel. 22, Last annotation update)
DE 30 kDa pollen allergen (Fragment).
GN GIX1.
OS Hordeum vulgare (Barley).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooidae;
OC Triticaceae; Hordeum.
OX NCBI_TaxId=4513;
RN [1]
RP SEQUENCE FROM N.A.
RA Astwood J.D.;
RT "Developmental and molecular characterization of pollen allergen
RT cognates in barley."
RL Thesis (1993), Plant Science, University of Manitoba.
RN [2]
RP SEQUENCE FROM N.A.
RA Astwood J.D.; Hill R.D.;
RT "Identification and expression of a high pI protein gene family in
RT barley pollen."
RL Plant Physiol. 102:10-10(1993).
RN [3]
RP SEQUENCE FROM N.A.
RA Astwood J.D.;
RL Submitted (FEB-1994) to the EMBL/GenBank/DBJ databases.
DR EMBL; U06640; AA16702.1; -.
DR InterPro; IPR001778; POA_allergenc.
DR InterPro; IPR002914; POA_allergenn.
DR Pfam; PF01620; Pollen_allerg_2; 1.
DR PRINTS; PR00833; POAALLERGEN.
FT NON TER
SQ SEQUENCE 179 AA; 18371 MW; 82D968F4F6EAECE CRC64;

Query Match 60.3%; Score 41; DB 10; Length 179;
Best Local Similarity 80.0%; Pred. No. 28;
Matches 8; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 3 AGTAPTAGNY 12
DB 166 AGAATAAGNY 177

RESULT 10
O9AG87 PRELIMINARY; PRT; 181 AA.
ID O9AG87;
AC O9AG87;
DT 01-JUN-2001 (TREMBlrel. 17, Created)
DT 01-JUN-2001 (TREMBlrel. 17, Last sequence update)
DT 01-JUN-2001 (TREMBlrel. 17, Last annotation update)
DE CsuA.
GN CsuA.
OS Vibrio parahaemolyticus.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Vibrionales;
OC Vibrionaceae; Vibrrio.
OX NCBI_TaxId=670;
RN [1]
RP SEQUENCE FROM N.A.
RA McCarter L.L.; Welsh C.; Boles B.;
RT "The csu locus of Vibrio parahaemolyticus."
RL Submitted (JAN-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF33087; AAK37520.1; -.
SQ SEQUENCE 181 AA; 18972 MW; 53CEEB43918CD09 CRC64;

Query Match 60.3%; Score 41; DB 2; Length 181;
Best Local Similarity 61.5%; Pred. No. 28;
Matches 8; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 1 KTAGTAPTAGNYS 13
DB 160 KAYGTSTAGNYS 172

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RESULT 11
O8T306 PRELIMINARY; PRT; 249 AA.
ID O8T306;
AC O8T306;
DT 01-JUN-2002 (TREMBlrel. 21, Created)
DT 01-JUN-2002 (TREMBlrel. 21, Last sequence update)
DT 01-MAR-2003 (TREMBlrel. 23, Last annotation update)
DE Helix-loop-helix transcription factor.
GN HAIRY.
OS Tribolium castaneum (Red flour beetle).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Coleoptera; Polyphaga; Cuculiformia;
OC Tenebrionidae; Tribolium.
OX NCBI_TaxId=7070;
RN [1]
RP SEQUENCE FROM N.A.
RA Eckert C.; Wolf C.; Wimmer E.; Tautz D.;
RT "Functional analysis of the regulatory region of the pair-rule gene
RT hairy in Tribolium suggests regulatory divergence inspite of conserved
RT expression."
RL Submitted (APR-2002) to the EMBL/GenBank/DBJ databases.
CC -1- SIMILARITY: BELONGS TO THE BASIC HELIX-LOOP-HELIX (BHLH) FAMILY OF
CC TRANSCRIPTION FACTORS.
DR EMBL; AJ457831; CAD29886.1; -.
DR InterPro; IPR001092; HLH_Basic.
DR InterPro; IPR003650; Orange.
DR Pfam; PF00010; HLH; 1.
DR SMART; SM00353; HLH; 1.
DR SMART; SM00511; ORANGE; 1.
DR PROSITE; PS00038; HLH_1; 1.
DR PROSITE; PS50888; HLH_2; 1.
SQ SEQUENCE 249 AA; 27252 MW; 364B299EBF429B CRC64;

Query Match 60.3%; Score 41; DB 5; Length 249;
Best Local Similarity 61.5%; Pred. No. 39;
Matches 8; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 1 KTAGTAPTAGNYS 13
DB 205 RTASTASASNYS 217

RESULT 12
O04828 PRELIMINARY; PRT; 313 AA.
ID O04828;
AC O04828;
DT 01-JUL-1997 (TREMBlrel. 04, Created)
DT 01-JUL-1997 (TREMBlrel. 04, Last sequence update)
DT 01-OCT-2002 (TREMBlrel. 22, Last annotation update)
DE Pollen allergen precursor.
GN HORV9.
OS Hordeum vulgare (Barley).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooidae;
OC Triticaceae; Hordeum.
OX NCBI_TaxId=4513;
RN [1]
RP SEQUENCE FROM N.A.
RA MEDLINE=97136690; PubMed=8982067;
RA Astwood J.D.; Hill R.D.;
RT "Cloning and expression pattern of Hor v 9, the group 9 pollen
RT isoallergen from barley."
RL Gene 182:53-62(1996).
DR EMBL; U57845; AAB41585.1; -.
DR InterPro; IPR001778; POA_allergenc.
DR InterPro; IPR002914; POA_allergenn.
DR Pfam; PF01620; Pollen_allerg_2; 1.
DR PRINTS; PR00833; POAALLERGEN.
KW SIGNAL.
FT CHAIN 28 313 POTENTIAL.
FT SIGNAL 28 313 POLLEN ALLERGEN.
SQ SEQUENCE 313 AA; 33147 MW; D6D174B5D3090005 CRC64;

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Query Match 60.3%; Score 41; DB 10; Length 313;  
 Best Local Similarity 80.0%; Pred. No. 50;  
 Matches 8; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 3 AGTAPTAGNY 12  
 DB 302 AGAATAGNY 311

## RESULT 13

Q94JTI PRELIMINARY; PRT; 560 AA.  
 AC Q94JTI;  
 DT 01-DEC-2001 (TREMBlrel. 19, Created)  
 DT 01-DEC-2001 (TREMBlrel. 19, Last sequence update)  
 DT 01-OCT-2002 (TREMBlrel. 22, Last annotation update)  
 DE ATG4240/MUB21\_12 (EC 5.3.1.9) (Glucose-6-phosphate isomerase) (GPI)  
 DE (Phosphoglucose isomerase) (PGI) (Phosphohexose isomerase)  
 DE (PHI)  
 OS Arabidopsis thaliana (Mouse-ear cress).  
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;  
 OC Eucosida II; Brassicales; Brassicaceae; Arabidopsis.  
 CX NCBI\_TaxID=3702;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RA Shin P., Chen H., Cheuk R., Kim C.J., Meyers M.C., Banh J.,  
 RA Bower L., Carninci P., Chung M.K., Goldsmith A.D., Hayashizaki Y.,  
 RA Ishida J., Jones T., Kamiya A., Karlin-Neumann G., Kawai J., Lam B.,  
 RA Lee J.M., Lin J., Liu S.X., Miranda M., Narusaka M., Nguyen M.,  
 RA Palm C.J., Pham P.K., Quach H.L., Sakano H., Sakurai T., Satou M.,  
 RA Seki M., Southwick A., Toriumi M., Yamada K., Yu G., Shinozaki K.,  
 RA Davis R.W., Theologis A., Ecker J.R.;  
 RT "Arabidopsis cDNA clones";  
 RL Submitted (APR-2001) to the EMBL/GenBank/DBJ databases.  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RA Cheuk R., Chen H., Kim C.J., Meyers M.C., Shin P., Banh J.,  
 RA Bower L., Carninci P., Chang E., Dale J.M., Goldsmith A.D.,  
 RA Hayashizaki Y., Ishida J., Jones T., Kamiya A., Karlin-Neumann G.,  
 RA Kawai J., Lam B., Lee J.M., Lin J., Miranda M., Narusaka M.,  
 RA Nguyen M., Onodera C.S., Palm C.J., Quach H.L., Sakurai T., Satou M.,  
 RA Seki M., Southwick A., Tang C.C., Toriumi M., Wu H.C., Yamada K.,  
 RA Yamamura Y., Yu G., Yu S., Shinozaki K., Davis R.W., Theologis A.,  
 RA Ecker J.R.;  
 RT "Arabidopsis ORF clones";  
 RL Submitted (APR-2002) to the EMBL/GenBank/DBJ databases.  
 CC -1- CATALYTIC ACTIVITY: D-GLUCOSE 6-PHOSPHATE = D-FRUCTOSE 6-PHOSPHATE.  
 CC -1- PATHWAY: INVOLVED IN GLYCOLYSIS AND IN GLUCONEOGENESIS.  
 CC -1- SUBCELLULAR LOCATION: CYTOPLASMIC (BY SIMILARITY).  
 CC -1- SIMILARITY: BELONGS TO THE GPI FAMILY.  
 DR EMBL; AF372970; AAK50107.1; -;  
 DR EMBL; AY093962; AAM16223.1; -;  
 DR InterPro; IPR001672; G6P\_Isomerase.  
 DR Pfam; PF00342; PGI; 1.  
 DR PRINTS; PR00662; G6PISOMERASE.  
 DR PROSITE; PS00765; P\_GLUCOSE\_ISOMERASE\_1; 1.  
 DR PROSITE; PS00174; P\_GLUCOSE\_ISOMERASE\_2; 1.  
 KW Glucosogenesis; Glycolysis; Isomerase.  
 SQ SEQUENCE 560 AA; 61657 MW; 0ACC69EB82A534CD CRC64;

Query Match 60.3%; Score 41; DB 10; Length 560;  
 Best Local Similarity 61.5%; Pred. No. 93;  
 Matches 8; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

QY 1 KTAGTAPTAGNY 13  
 DB 531 RTGTAPEGPNYS 543

## RESULT 14

ID Q8WSZ4 PRELIMINARY; PRT; 573 AA.  
 AC Q8WSZ4;  
 DT 01-OCT-2002 (TREMBlrel. 22, Created)  
 DT 01-OCT-2002 (TREMBlrel. 22, Last sequence update)  
 DT 01-MAR-2003 (TREMBlrel. 23, Last annotation update)  
 DE GWO7509P.  
 GN LARP OR CG14066.  
 OS Drosophila melanogaster (fruit fly).  
 OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;  
 OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;  
 OC Ephydroidea; Drosophilidae; Drosophila.  
 CX NCBI\_TaxID=7227;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RA Stapleton M., Brokstein P., Hong L., Agbayani A., Carlson J.,  
 RA Champe M., Chavez C., Doreak V., Dresnek D., Fafan D., Frise E.,  
 RA George R., Gonzalez M., Guarin H., Krommler B., Li P., Liao G.,  
 RA Miranda A., Mungall C.J., Nunoo J., Pacleb J., Paragas V., Park S.,  
 RA Patel S., Phouanavong S., Wan K., Yu C., Lewis S.E., Rubin G.M.,  
 RA Ceollier S.;  
 RL Submitted (JUN-2002) to the EMBL/GenBank/DBJ databases.  
 DR EMBL; AY118468; AAM49837.1; -;  
 DR FlyBase; FBgn0040108; larp.  
 DR InterPro; IPR006607; DPF\_DM15.  
 DR SMART; SM00684; DM15; 3.  
 SQ SEQUENCE 573 AA; 64261 MW; E3637D6759D9BFF CRC64;

Query Match 60.3%; Score 41; DB 5; Length 573;  
 Best Local Similarity 63.6%; Pred. No. 95;  
 Matches 7; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 2 TAGTAPTAGNY 12  
 DB 205 SAGTSPTSSSY 215

RESULT 15  
 Q8CG10 PRELIMINARY; PRT; 672 AA.  
 ID Q8CG10;  
 DT 01-MAR-2003 (TREMBlrel. 23, Created)  
 DT 01-MAR-2003 (TREMBlrel. 23, Last sequence update)  
 DT 01-MAR-2003 (TREMBlrel. 23, Last annotation update)  
 DE Fork head-related protein like A.  
 GN MFKHLA.  
 OS Mus musculus (Mouse).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 CX NCBI\_TaxID=10090;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RA Daigo Y., Takayama I., Fujino M.A.;  
 RT "Isolation and characterization of novel human and mouse genes, which  
 are expressed in the digestive tract";  
 RL Submitted (DEC-2000) to the EMBL/GenBank/DBJ databases.  
 DR EMBL; AB052766; BAC53799.1; -;  
 SQ SEQUENCE 672 AA; 72758 MW; 8B89F59EF85FC768 CRC64;

Query Match 60.3%; Score 41; DB 11; Length 672;  
 Best Local Similarity 88.9%; Pred. No. 1.1e+02;  
 Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 TAGTAPTAG 10  
 DB 35 TAGTAPAG 43

Search completed: February 6, 2004, 11:40:13  
 Job time : 37 sec

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## Refine Search

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### Search Results -

Terms	Documents
5705197.pn.	1

Database:

US Pre-Grant Publication Full-Text Database  
 US Patents Full-Text Database  
 US OCR Full-Text Database  
 EPO Abstracts Database  
 JPO Abstracts Database  
 Derwent World Patents Index  
 IBM Technical Disclosure Bulletins

Search:

L7






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### Search History

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**Set Name Query**

side by side

**Hit Count Set Name**

result set

DB=USPT; PLUR=YES; OP=OR

<u>L7</u>	5705197.pn.	1	<u>L7</u>
<u>L6</u>	5693343.pn.	1	<u>L6</u>
<u>L5</u>	L4 and l3	7	<u>L5</u>
<u>L4</u>	CFA/I	48	<u>L4</u>
<u>L3</u>	biocompatible and L2	3595	<u>L3</u>
<u>L2</u>	L1 and biodegradable microphere	12076	<u>L2</u>
<u>L1</u>	burst-free programmable sustained release	642821	<u>L1</u>

END OF SEARCH HISTORY

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## Refine Search

### Search Results -

Terms	Documents
L4 and L3	7

Database:

US Pre-Grant Publication Full-Text Database  
 US Patents Full-Text Database  
 US OCR Full-Text Database  
 EPO Abstracts Database  
 JPO Abstracts Database  
 Derwent World Patents Index  
 IBM Technical Disclosure Bulletins

Search:

L5

Refine Search

Recall Text

Clear

Interrupt

### Search History

DATE: Friday, February 06, 2004 [Printable Copy](#) [Create Case](#)

#### Set Name Query

side by side

DB=USPT; PLUR=YES; OP=OR

#### Hit Count Set Name

result set

<u>L5</u>	L4 and l3	7	<u>L5</u>
<u>L4</u>	CFA/I	48	<u>L4</u>
<u>L3</u>	biocompatible and L2	3595	<u>L3</u>
<u>L2</u>	L1 and biodegradable microsphere	12076	<u>L2</u>
<u>L1</u>	burst-free programmable sustained release	642821	<u>L1</u>

END OF SEARCH HISTORY

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Search Results - Record(s) 1 through 7 of 7 returned.

☐ 1. Document ID: US 6531156 B1

L5: Entry 1 of 7

File: USPT

Mar 11, 2003

US-PAT-NO: 6531156

DOCUMENT-IDENTIFIER: US 6531156 B1

TITLE: Aqueous solven encapsulation method, apparatus and microcapsules

DATE-ISSUED: March 11, 2003

## INVENTOR-INFORMATION:

NAME	CITY	STATE	ZIP CODE	COUNTRY
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US-CL-CURRENT: [424/489](#); [426/490](#), [426/492](#), [426/496](#), [426/497](#), [426/499](#), [426/500](#)

<a href="#">Full</a>	<a href="#">Title</a>	<a href="#">Citation</a>	<a href="#">Front</a>	<a href="#">Review</a>	<a href="#">Classification</a>	<a href="#">Date</a>	<a href="#">Reference</a>	<a href="#">Sequences</a>	<a href="#">Attachments</a>	<a href="#">Claims</a>	<a href="#">KWC</a>	<a href="#">Draw. D</a>
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☐ 2. Document ID: US 6528097 B1

L5: Entry 2 of 7

File: USPT

Mar 4, 2003

US-PAT-NO: 6528097

DOCUMENT-IDENTIFIER: US 6528097 B1

TITLE: Sustained release non-steroidal, anti-inflammatory and lidocaine PLGA microspheres

DATE-ISSUED: March 4, 2003

## INVENTOR-INFORMATION:

NAME	CITY	STATE	ZIP CODE	COUNTRY
Vaughn; William M.	Silver Spring	MD		
Van Hamont; John E.	Ft. Meade	MD		
Setterstrom; Jean A.	Alpharetta	GA		

US-CL-CURRENT: [424/501](#); [424/422](#), [514/570](#)

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Full	Title	Citation	Front	Review	Classification	Date	Reference	Sequences	Attachments	Claims	KWIC	Draw. De
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☐ 3. Document ID: US 6447796 B1

L5: Entry 3 of 7

File: USPT

Sep 10, 2002

US-PAT-NO: 6447796

DOCUMENT-IDENTIFIER: US 6447796 B1

**\*\* See image for Certificate of Correction \*\***TITLE: Sustained release hydrophobic bioactive PLGA microspheres

DATE-ISSUED: September 10, 2002

## INVENTOR-INFORMATION:

NAME	CITY	STATE	ZIP CODE	COUNTRY
Vook; Noelle Christine	Schaumburg	IL		
Jacob; Elliott	Silver Spring	MD		
Setterstrom; Jean A.	Alpharetta	GA		
van Hamont; John	West Point	NY		
Vaughan; William	Silver Spring	MD		
Duong; Ha	Montclair	CA		

US-CL-CURRENT: 424/422; 424/426, 424/457, 424/468

Full	Title	Citation	Front	Review	Classification	Date	Reference	Sequences	Attachments	Claims	KWIC	Draw. De
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☐ 4. Document ID: US 6410056 B1

L5: Entry 4 of 7

File: USPT

Jun 25, 2002

US-PAT-NO: 6410056

DOCUMENT-IDENTIFIER: US 6410056 B1

TITLE: Chemotherapeutic treatment of bacterial infections with an antibiotic encapsulated within a biodegradable polymeric matrix

DATE-ISSUED: June 25, 2002

## INVENTOR-INFORMATION:

NAME	CITY	STATE	ZIP CODE	COUNTRY
Setterstrom; Jean A.	Silver Spring	MD		
Jacob; Elliot	Silver Spring	MD		
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US-CL-CURRENT: 424/501; 424/502, 428/402.24, 514/772.3

Full	Title	Citation	Front	Review	Classification	Date	Reference	Sequences	Attachments	Claims	KWIC	Draw. De
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☐ 5. Document ID: US 6309669 B1

L5: Entry 5 of 7

File: USPT

Oct 30, 2001

US-PAT-NO: 6309669

DOCUMENT-IDENTIFIER: US 6309669 B1

TITLE: Therapeutic treatment and prevention of infections with a bioactive materials encapsulated within a biodegradable-biocompatible polymeric matrix

DATE-ISSUED: October 30, 2001

## INVENTOR-INFORMATION:

NAME	CITY	STATE	ZIP CODE	COUNTRY
Setterstrom; Jean A.	Alpharetta	GA		
Van Hamont; John E.	Fort Meade	MD		
Reid; Robert H.	McComas	CT		
Jacob; Elliot	Silver Spring	MD		
Jeyanthi; Ramasubbu	Columbia	MD		
Boedeker; Edgar C.	Chevy Chase	MD		
McQueen; Charles E.	Olney	MD		
Jarboe; Daniel L.	Silver Spring	MD		
Cassels; Frederick	Ellicott City	MD		
Brown; William	Denver	CO		
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Roberts; F. Donald	Dover	MA		
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US-CL-CURRENT: 424/486; 424/422, 424/423, 424/424, 424/425, 424/484

Full	Title	Citation	Front	Review	Classification	Date	Reference	Sequences	Attachment	Claims	KMC	Draw. De
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☐ 6. Document ID: US 6217911 B1

L5: Entry 6 of 7

File: USPT

Apr 17, 2001

US-PAT-NO: 6217911

DOCUMENT-IDENTIFIER: US 6217911 B1

**\*\* See image for Certificate of Correction \*\***

TITLE: sustained release non-steroidal, anti-inflammatory and lidocaine PLGA microspheres

DATE-ISSUED: April 17, 2001

## INVENTOR-INFORMATION:

NAME	CITY	STATE	ZIP CODE	COUNTRY
Vaughn; William M.	Silver Spring	MD		

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Van Hamont; John E.                      Ft. Meade                      MD  
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US-CL-CURRENT: 424/501; 424/422, 514/570

Full	Title	Citation	Front	Review	Classification	Date	Reference	Sequences	Attachments	Claims	KWIC	Drawings
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☐ 7. Document ID: US 5417986 A

L5: Entry 7 of 7

File: USPT

May 23, 1995

US-PAT-NO: 5417986

DOCUMENT-IDENTIFIER: US 5417986 A

TITLE: Vaccines against diseases caused by enteropathogenic organisms using antigens encapsulated within biodegradable-biocompatible microspheres

DATE-ISSUED: May 23, 1995

INVENTOR-INFORMATION:

NAME	CITY	STATE	ZIP CODE	COUNTRY
Reid; Robert H.	Kensington	MD		
Boedeker; Edgar C.	Chevy Chase	MD		
van Hamont; John E.	Shape			BE
Setterstrom; Jean A.	Takoma Park	MD		

US-CL-CURRENT: 424/499; 424/422, 424/426, 424/433, 424/444, 424/455, 424/470,  
424/486, 424/488, 424/489, 424/491

Full	Title	Citation	Front	Review	Classification	Date	Reference	Sequences	Attachments	Claims	KWIC	Drawings
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L5: Entry 2 of 7

File: USPT

Mar 4, 2003

DOCUMENT-IDENTIFIER: US 6528097 B1

TITLE: Sustained release non-steroidal, anti-inflammatory and lidocaine PLGA microspheresAbstract Text (1):

A controlled release microcapsule pharmaceutical formulation for burst-free, sustained, programmable release of a non-steroidal, antiinflammatory drug over a duration from 24 hours to 2 months, comprising: a non-steroidal, antiinflammatory drug and a blend of biocompatible, biodegradable poly (lactide/glycolide).

Brief Summary Text (2):

This invention relates to providing novel pharmaceutical compositions for local delivery and sustained release of non-steroidal, anti-inflammatory drugs (NSAIDS) from biocompatible, biodegradable poly(DL-lactide-co-glycolide) (PLGA) microspheres. The resulting product is applied locally into soft tissues surrounding a surgical incision or traumatic wound site where it will locally sustain release of the NSAID.

Brief Summary Text (3):

The invention also relates to providing novel pharmaceutical compositions for local delivery and sustained release of lidocaine PLGA microspheres.

Brief Summary Text (5):

Non-steroidal anti-inflammatory drugs (NSAIDS) have been effective in reducing inflammation and inducing analgesia; however, the conventional oral dosage forms of these drugs characteristically have short half-lives and irritate the gastrointestinal mucosa. Further, currently available slow release oral dosage forms, such as Biovail (enteric coated, double-layer tablets which release the drug for 12-24 hours) still result in inefficient systemic delivery of the drug and potential gastrointestinal irritation.

Brief Summary Text (6):

Therefore, currently available slow release oral dosage forms of NSAIDs induces systemic effects and the drug is not efficiently used at the site of inflammation.

Brief Summary Text (7):

Further, in the currently available slow release oral dosage forms of NSAIDs, fillers or additives are needed in order to accelerate or retard drug release.

Brief Summary Text (9):

Several publications and patents are available for sustained release of active agents from biodegradable polymers, particularly, poly(lactide/glycolides) (PLGA). Prior usages of PLGA for controlled release of polypeptides have involved the use of molar ratios of lactide/glycolide (L/G) of 75/25 to 100/0 for molecular weights >20,000. Further, prior art preparations of PLGA utilized fillers or additives in the inner aqueous layer to improve stability and encapsulation efficiency and/or to increase the viscosity of the aqueous layer, thereby modulating polymer hydrolysis and the biologically active agent or polypeptide release.

Brief Summary Text (10):

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In addition, the prior art use of PLGA copolymers were end-capped, in that the terminal carboxyl end groups were blocked. In these end-capped co-polymers, the microcapsule preparations exhibited a low to moderate burst release of .about.10-14% of the entrapped polypeptide in the first 24 hours after placement in an aqueous physiological environment. In part, these characteristics are due to the use of fillers in the inner aqueous phase. Further, a 1-month release of polypeptide is known with the use of a 75/25 co-polymer of PLGA of Mw <20,000.

Brief Summary Text (11):

Investigations in controlled release research has been proceeding especially to obtain a 1-2 month delivery system for biologically active agents or polypeptides using poly(lactide/glycolide) polymers. However, most of these systems have one or more of the following problems: poor encapsulation efficiency and large 'burst release' followed by an intermediate 'no release' or 'lag phase' until the polymer degrades. In general, release from these polymers occur over a period from about 4 weeks to about several months. In addition, in order to achieve this release a 50/50 co-polymer of Mw>30,000 or a 75/25 co-polymer of Mw>10,000 are employed which often results in residual polymer remaining at the site of administration long after the release of active core.

Brief Summary Text (13):

This invention provides novel pharmaceutical compositions for local delivery and sustained release of non-steroidal, anti-inflammatory drugs (NSAIDs) from biocompatible, biodegradable poly(DL-lactide-co-glycolide) (PLGA) microspheres. The resulting product is applied locally into soft tissues surrounding a surgical incision or traumatic wound site where it will locally sustain release the NSAID. In the context of this invention, ketoprofen, is preferred. Ketoprofen is an important non-steroidal anti-inflammatory drug, and is formulated into a drug delivery system that releases the drug in an aqueous solution or soft tissue for 7-60 days, depending upon its formulation.

Brief Summary Text (14):

The invention also provides novel pharmaceutical compositions for local delivery and sustained release of lidocaine PLGA microspheres.

Brief Summary Text (15):

One object of the invention is to provide biodegradable PLGA microspheres for sustained delivery of NSAIDs.

Brief Summary Text (16):

Another object of the invention is to provide sustained, local delivery of NSAIDs, for durations greater than 24 hours and for up to 2 months from a single dose.

Brief Summary Text (19):

A yet further object of the invention is to provide oral dosage forms incorporating compositions of NSAID-loaded microspheres of this invention to deliver the microspheres to the gastrointestinal lumen where they can be adsorbed within the epithelium and sustain release their contents systemically.

Brief Summary Text (21):

A further object yet still is to provide sustained released lidocaine PLGA microspheres for the treatment of dental pain.

Brief Summary Text (24):

In the solvent evaporation process, the NSAID and PLGA were dissolved in a volatile organic solvent, preferably methylene chloride, and dispersed in an aqueous phase containing an emulsion stabilizer. Evaporation of the organic phase gave NSAID-loaded microspheres. Depending on processing parameters, the microspheres released the NSAID for a duration of 2 weeks to 2 months with minimal burst release.

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Drawing Description Text (4):

FIG. 3 shows ketoprofen release profiles from PLGA microspheres prepared by solvent evaporation. The release profiles are biphasic with a slower release in the first week followed by a more rapid release during the second week.

Drawing Description Text (5):

FIG. 4 shows ketoprofen release profiles from PLGA microspheres prepared by solvent evaporation with increased initial polymer concentrations. A zero-order release of ketoprofen over 33 days is obtained. WV51a was prepared at reduced PLGA concentrations.

Drawing Description Text (6):

FIG. 5 shows ketoprofen release profiles from PLGA microspheres prepared by solvent evaporation at 40.degree. C. demonstrating a zero-order release of 40-60% of the loaded ketoprofen followed by a terminal burst release of the remaining drug. WV29 was prepared at 20.degree. C.

Drawing Description Text (7):

FIG. 6 shows ketoprofen release profiles from PLGA microspheres prepared by solvent extraction demonstrating 7-10 day release.

Drawing Description Text (10):

FIG. 9 shows release profiles of lidocaine-PLGA microspheres prepared by solvent evaporation.

Drawing Description Text (11):

FIG. 10 shows release profiles of lidocaine hydrochloride PLGA formulations prepared by solvent extraction.

Detailed Description Text (2):

This invention relates to the design of biocompatible and biodegradable microspheres for novel, sustained release of non-steroidal, anti-inflammatory drugs, including ketoprofen, over a period of up to 60 days in an aqueous physiological environment with little or no burst release.

Detailed Description Text (3):

Unlike currently available release systems which rely on the use of filler/additives such as gelatin, albumin, dextran, pectin, polyvinyl pyrrolidone, polyethylene glycol, sugars, etc., and are still prone to low encapsulation efficiencies and "burst effects", this invention achieves high encapsulation efficiency and 'burst-free' release without the use of any additive. In this invention, 'burst-free', programmable sustained release is achieved.

Detailed Description Text (5):

Additionally, two forms of the biocompatible, biodegradable poly(DL-/lactide-shield-glycolide) can be employed, one being the more hydrophobic end-capped polymer with the terminal residues functionalized as esters, and the other being the more hydrophilic uncapped polymer with the terminal residues existing as carboxylic acids.

Detailed Description Text (8):

Ketoprofen and PLGA were dissolved in methylene chloride, and dispersed in an aqueous phase containing an emulsion stabilizer. Evaporation of the organic phase gave ketoprofen-loaded microspheres, as is shown in FIGS. 1, 3, 4, and 5. The microspheres release ketoprofen for a duration of two weeks to two months with minimal burst release as can be seen from the foregoing referred to figures.

Detailed Description Text (11):

In the solvent extraction process, ketoprofen and PLGA were dissolved in acetonitrile, which is a polar organic solvent, and the mixture of ketoprofen, PLGA

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and acetonitrile is then dispersed in a mineral oil; however, any non-polar organic phase other than mineral oil will suffice in the context of the invention, even though mineral oil is preferred. The emulsion produced is then poured into a hydrocarbon solvent, preferably heptane. As the mineral oil phase was extracted into the heptane, microspheres of PLGA and ketoprofen are formed. The microspheres produced release ketoprofen for seven to ten days displaying near zero-order kinetics. Microspheres produced using this solvent extraction process are shown in FIGS. 2 and 6.

Detailed Description Text (13):

The NSAIDs are prescribed for arthritic conditions to reduce pain and delay debilitating inflammation, and a single, localized dose into joints lasting 2-3 months is very advantageous. Further, the microspheres of the invention are suitable for incorporation into a number of delivery vehicles to provide sustained release of a NSAID-loaded for many other applications for the treatment of mild pain and inflammation.

Detailed Description Text (22):

Ketoprofen release profiles were determined in vitro for the PLGA microspheres. Microspheres were suspended in 1 ml phosphate buffer solution maintained at 37.+- .1.degree. C. in a shaker bath. The buffer was removed and refreshed over time. The ketoprofen concentration was determined by HPLC.

Detailed Description Text (27):

Characteristically, ketoprofen-PLGA microspheres prepared by solvent evaporation slowly released 25-35% of their contents during the first week. This release was followed by an accelerated release of the remaining drug during the next 7-10 days. After 50 days, the hydrated microspheres had not significantly degraded.

Detailed Description Text (28):

Factors contributing to the lag time before significant release was observed include the high molecular weight (70k-100k g/mol) and hydrophobic nature of the PLGA resulting in slow hydration of the microspheres. Also, SEM analysis showed product spheres to be relatively free of defects reducing the possibility of a burst release. Similar profiles of an accelerated release beginning at 7-10 days were observed for lidocaine-PLGA formulations with the same polymer molecular weight. Release is independent of the core loading for this narrow range of 1.5-13.5%.

Detailed Description Text (29):

Heated solvent evaporation formulations (core loads: 7.6, 7.3%) demonstrate zero-order, more sustained release. At 30 days, only 30% of the ketoprofen is estimated to be released.

Detailed Description Text (30):

Ketoprofen-PLGA formulations prepared by solvent extraction show a steady and complete release of ketoprofen in 7-10 days (FIG. 6). The increased surface area of these smaller diameter microspheres contribute to the observed release. The near-linear release indicates the drug is evenly distributed throughout the PLGA matrix. Such release characteristics are highly beneficial for use as anti-inflammatory pulp-capping materials.

Detailed Description Text (31):

Ketoprofen and PLGA combined to form a miscible and homogeneous solid matrix of drug microspheres. This result affords steady and sustained ketoprofen release vehicles for potential use for localized inflammation. In relation to the treatment of pulpitis, plastic chambers are being used to model interactions between ketoprofen and dentin, inflamed pulpal tissue, and common pulp capping dressings such as calcium hydroxide.

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Detailed Description Text (35):

This study proposes to evaluate the safety, analgesic efficacy, and tissue response of locally applied ketoprofen [a non steroidal anti-inflammatory drug (NSAID)] that is encapsulated within small microspheres of the biodegradable polymer poly DL (lactide-co-glycolide). The response to encapsulated ketoprofen will be compared to a long-acting local anesthetic such as tetracaine, lidocaine, etidocaine, carbocaine, xylocaine, marcaine, nesacaine and etiod. Both drug formulations will be instilled into post-extraction sites immediately upon extraction of the tooth, but prior to the onset of pain (patients will be under the influence of local anesthetic during the extraction procedure). Subjects (n=84) will have two mandibular impacted third molars removed and be randomly allocated to receive one of six possible treatments placed into the resulting sockets: 0 mg (placebo formation), 3.125 mg, 6.25 mg, or 25 mg ketoprofen, or 50 mg bupivacaine. Each patient in these six groups (n=12/group) will also receive an oral placebo capsule. The seventh group of the subjects will receive a placebo applied at the extraction sites and 25 mg of ketoprofen orally. Subjects will remain at the clinic for six hours following drug administration. Every 30 minutes the offset of mandibular anesthesia, postoperative pain intensity, side effects, and recurrence of bleeding will be monitored. Demonstration of a dose-response relationship for ketoprofen at doses lower than needed for analgesia following oral administration will provide the basis for a follow-up study in which an optimal dose of ketoprofen will be combined with bupivacaine.

Detailed Description Text (38):

The introduction of NSAIDs for the management of acute and chronic pain has resulted in improved analgesia and decreased side effects; however, there remain drawbacks such as a relatively slow therapeutic onset when taken orally, a ceiling of efficacy, and side effects with chronic use (NSAIDs will produce small amounts of GI bleeding at therapeutic doses which can result in ulcers with chronic use in approximately 25% of individuals). An alternative to administering high systematic doses for greater efficacy and a likely way to eliminate side effects is to sustain release NSAIDs or other drugs at the site of injury thereby achieving high local concentrations. This proposed study will evaluate the local administration of an NSAID into tooth extraction sites to determine if such a localized effect can be demonstrated. If demonstrated, it will provide a basis for evaluating the peripheral effects of other putative inhibitors and antagonists of the inflammatory process using this or a similar approach. Despite advantages of NSAIDs for pain management, a therapeutic void remains for the management of pain with a drug modality that has rapid onset by non-parenteral routes of administration and greater efficacy than can be achieved with oral NSAIDs.

Detailed Description Text (55):

Adverse Effects of Microencapsulated Ketoprofen: The adverse effects attributed to orally administered ketoprofen are similar to those associated with other NSAIDs: GI irritation and upset, and impairment of renal function with chronic administration. Administration of ketoprofen (the free drug form) into extraction sites in two previous studies done at NIDR was not associated with any detectable increase in localized adverse effects such as alveolar osteitis or infection in 50 subjects.<sup>sup.1,2</sup> It is recognized that the administration of an NSAID into the extraction site prior to blood clot formation may result in an increase in postoperative bleeding due to the temporary inhibitory effects of NSAIDs on platelet aggregation. Direct administration of 30 mg of aspirin into the extraction sites following oral surgery has been reported not to produce any increase in bleeding episodes or alveolar osteitis.<sup>sup.3</sup> Subjects will be observed for any signs of bleeding during the six hour observation period and prior to dismissal from the clinic. The presense of the encapsulation excipient DL (lactide-co-glycolide) may possibly be associated with an increase in the infection rate; however, since it is the same polymer used in biodegradable suture materials (which have a very low infection rate in other surgeries), it is considered unlikely.

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Detailed Description Text (71):

Lidocaine release profiles were determined in vitro for the PLGA microspheres. Microspheres were suspended in a phosphate buffer solution maintained at 37.+- .1.degree. C. in a shaker bath, and aliquots were taken during the release period. The lidocaine concentration was determined by HPLC as stated above.

Detailed Description Text (74):

Cumulative release profiles for solvent evaporation and solvent extraction formulations are shown in FIGS. 9 and 10, respectively. In FIG. 9, lidocaine-PLGA microspheres prepared by solvent evaporation slowly released 5-15% of their contents during the first week. This release was followed by a continuous release during the initial stages. After 60 days, the hydrated microspheres had not significantly degraded. Factors contributing to the lag time before significant release was observed include the high molecular weight (70k-100k) g/mol) and hydrophobic nature of PLGA resulting in slow hydration of the microspheres. Also, SEM analysis showed product spheres to be relatively free of defects reducing the possibility of a burst release.

Detailed Description Text (75):

In FIG. 10, lidocaine hydrochloride-PLGA formulations prepared by solvent extraction essentially dumped 70-90% of their core load in the first 24 hours with complete release within days. The increased surface area of these smaller diameter microspheres and their high surface porosity observed by SEM contribute to the observed release, as well as the high aqueous solubility of the incipient lidocaine hydrochloride. It appears that lidocaine hydrochloride is mostly surface-bound in the microsphere formulations rather than homogeneously distributed throughout the polymer matrix.

Detailed Description Text (76):

Sustained release formulations releasing the. anesthetic lidocaine have been prepared by o/w solvent.evaporation techniques resulting in continuous release for 7-10 days following a one week, burst-free lag time. Conversely, lidocaine hydrochloride-PLGA formulations prepared by w/o solvent extraction completely emptied their contents within the first few days.

Other Reference Publication (1):

Gilding, Biodegradable polymers for use in surgery-polyglycolic/poly (ac c acid) homo-and copolymers: 1, Polymer, vol. 20, Dec. 1979, pp1459-1464.

Other Reference Publication (6):

Jeyanthi, et al., Novel, Burst Free Programmable Biodegradable Microspheres For Controlled Release of Polypeptides, Proceedings Int. Symp. control Release Bioact. Mater. (1996) p351-352.

Other Reference Publication (7):

Yeh, A novel emulsification-solvent extraction technique for production of protein loaded biodegradable microparticles for vaccine and drug delivery, Journal of Controlled Release, 33 (1995) 437-445.

Other Reference Publication (8):

Yan, Characterization and morphological analysis of protein-loaded poly(lactide-co-glycolide) microparticles prepared by water-in-oil-in-water emulsion technique, Journal of Controlled Release, 32 (1994) 231-241.

Other Reference Publication (9):

Wang, et al., Influence of formulation methods on the in vitro controlled release of protein from poly (ester) microspheres Journal of Controlled Release, 17 (1991) 23-32.

Other Reference Publication (11):

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Setterstrom, Controlled Release of Antibiotics From biodegradable Microcapsules For Wound infection Control, Chemical Abstracts, 1983, pp215-226.

Other Reference Publication (15):

McConnel, et al., Antigenic homology within human enterotoxigenic Escherichia coli fimbrial colonization factor antigens: CFA/I, coli-surface-associated antigens (CS) 1, CS2, CS4 and CS17, FEMS Microbiology Letters 61 (1989) 105-108.

CLAIMS:

1. A process for preparing controlled release microcapsule formulations characterized by burst-free, sustained, programmable release of non-steroidal, antiinflammatory drugs comprising: dissolving a non-steroidal, antiinflammatory drug and a mixture of uncapped biocompatible, biodegradable poly(lactide/glycolide) polymer and end-capped biocompatible, biodegradable poly(lactide/glycolide) polymer in a volatile organic solvent, dispersing the dissolved mixture in an aqueous phase containing an emulsion stabilizer, and evaporating the organic solvent phase to obtain non-steroidal antiinflammatory drug-loaded microspheres.

2. A process for preparing controlled release microcapsule formulations characterized by burst-free, sustained, programmable release of non-steroidal, antiinflammatory drugs comprising: dissolving a non-steroidal, antiinflammatory drug and a mixture of uncapped biocompatible, biodegradable poly(lactide/glycolide) polymer and end-capped biocompatible, biodegradable poly(lactide/glycolide) polymer in a polar organic solvent, dispersing the dissolved non-steroidal, antiinflammatory drug dissolved in a polar organic solvent in a non-polar organic phase, pouring the emulsion into a hydrocarbon solvent, extracting the polar organic phase into the hydrocarbon solvent to form microspheres.

3. A process of preparing a controlled release microcapsule formulation characterized by burst-free sustained programmable release of a long-acting local anesthetic comprising: dissolving the long-acting local anesthetic and a mixture of uncapped biocompatible, biodegradable poly(lactide/glycolide) polymer and end-capped biocompatible, biodegradable poly(lactide/glycolide) polymer in a volatile organic solvent, dispersing the long-acting local anesthetic and volatile organic solvent in an aqueous phase containing an emulsion stabilizer, and evaporating the volatile organic solvent to precipitate microspheres of long-lasting local anesthetic and poly(lactide/glycolide) microspheres.

4. The process of claim 1, wherein the biodegradable poly(lactide/glycolide) polymers comprise a ratio of lactide to glycolide from 100/0 to 50/50.

12. The process of claim 2, wherein the biodegradable poly(lactide/glycolide) polymers comprise a ratio of lactide to glycolide from 100/0 to 50/50.

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